

# SCORE Search Results Details for Application 08819669 and Search Result us-08-819-669e-8.rni.

<a href="#">Score Home Page</a>	<a href="#">Retrieve Application List</a>	<a href="#">SCORE System Overview</a>	<a href="#">SCORE FAQ</a>	<a href="#">Comments / Suggestions</a>
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2006, 10:12:34 ; Search time 930 Seconds  
(without alignments)  
11415.776 Million cell updates/sec

Title: US-08-819-669E-8  
Perfect score: 5674  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_NA:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5674	100.0	5674	2	US-08-190-411A-1	Sequence 1, Appli
3	5674	100.0	5674	2	US-08-299-849B-8	Sequence 8, Appli
4	5674	100.0	5674	2	US-08-560-024-1	Sequence 1, Appli
5	5674	100.0	5674	2	US-08-142-368A-8	Sequence 8, Appli
6	5674	100.0	5674	3	US-08-967-727-8	Sequence 8, Appli
7	5674	100.0	5674	3	US-08-037-230D-8	Sequence 8, Appli
8	5674	100.0	5674	3	US-09-583-850-8	Sequence 8, Appli
9	5674	100.0	5674	3	US-09-579-197-8	Sequence 8, Appli
10	5674	100.0	5674	3	US-09-404-026-8	Sequence 8, Appli
11	5674	100.0	5674	3	US-09-312-464-8	Sequence 8, Appli
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14	3934.8	69.3	5699	3	US-09-949-016-14430	Sequence 14430, A
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17	2429.6	42.8	4736	3	US-09-056-105-12	Sequence 12, Appl
18	2422.8	42.7	4741	3	US-09-056-105-11	Sequence 11, Appl
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45	1762.6	31.1	4204	3	US-09-056-105-6	Sequence 6, Appli

#### ALIGNMENTS

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RESULT 1
US-07-807-043B-8
; Sequence 8, Application US/07807043B
; Patent No. 5342774
; GENERAL INFORMATION:
; APPLICANT: Boon, Thierry, Van den Eynde, Beno t
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor

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; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/807,043B
; FILING DATE: 19911212
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-May-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5342774man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 253.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: singular
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
US-07-807-043B-8

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Query Match          100.0%;  Score 5674;  DB 2;  Length 5674;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 5674;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
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Qy    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
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Db	481		CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
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Db	961		CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
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Db	1021		TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081		GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140

Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
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Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
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Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
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Qy	1321	CCCACCTCATCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
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Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
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Db	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
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Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040

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Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
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Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
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Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGATGTCT	2580
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Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTCAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTCAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
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Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940

Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
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Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
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Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTTCCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTTCCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
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Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
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Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
Db	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
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Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
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Db	3841	 CCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
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Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	 GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	 TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGC	4320
Db	4261	 AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	 CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	 CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	 GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	 CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCATATGGGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	 GGAGCACAGTGCCATATGGGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621	 GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	 CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800

Db	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACCTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACCTGAGCA	5400
Qy	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAAC	5460
Db	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAAC	5460
Qy	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Db	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Qy	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Db	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Qy	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCT	5640
Db	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCT	5640
Qy	5641	GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674
Db	5641	GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674

RESULT 2  
 US-08-190-411A-1  
 ; Sequence 1, Application US/08190411A  
 ; Patent No. 5541104  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chen, Yao-Tseng; Stockert, Elisabeth;  
 ; APPLICANT: Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.;  
 ; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry;  
 ; APPLICANT: Old, Lloyd J.  
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH BIND TO  
 ; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSOR MAGE-1, RECOMBINANT MAGE-1  
 ; TITLE OF INVENTION: AND MAGE-1 DERIVED IMMUNOGENIC PEPTIDES  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Felte & Lynch  
 ; STREET: 805 Third Avenue  
 ; CITY: New York City  
 ; STATE: New York  
 ; ZIP: 10022  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
 ; COMPUTER: IBM  
 ; OPERATING SYSTEM: PC-DOS  
 ; SOFTWARE: Wordperfect  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/190,411A  
 ; FILING DATE: 01-FEBRUARY-1994  
 ; CLASSIFICATION: 436  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 037,230  
 ; FILING DATE: 26-MARCH-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US92/04354  
 ; FILING DATE: 22-MAY-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/807,043  
 ; FILING DATE: 12-DECEMBER-1991  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/764,364  
 ; FILING DATE: 23-SEPTEMBER-1991  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/728,838  
 ; APPLICATION NUMBER: 9-JULY-1991  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/705,702  
 ; FILING DATE: 23-MAY-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Hanson, No. 5541104man D.  
 ; REGISTRATION NUMBER: 30,946  
 ; REFERENCE/DOCKET NUMBER: LUD 5354  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 688-9200  
 ; TELEFAX: (212) 838-3884  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5674 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear



; MOLECULE TYPE: genomic DNA  
; FEATURE:  
; NAME/KEY: MAGE-1 gene  
US-08-190-411A-1

Query Match 100.0%; Score 5674; DB 2; Length 5674;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CCCGGGGCACCACTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC	60
Db	1	CCCGGGGCACCACTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC	60
Qy	61	ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG	120
Db	61	ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG	120
Qy	121	CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG	180
Db	121	CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG	180
Qy	181	TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Db	181	TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Qy	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Db	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Qy	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Db	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Qy	361	TCAGGCTGGGCCACCCCAAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Db	361	TCAGGCTGGGCCACCCCAAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Qy	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Db	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Qy	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Db	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Qy	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Db	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Qy	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Db	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Qy	661	CACCCCCACCCCAACCCCAACGCCCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Db	661	CACCCCCACCCCAACCCCAACGCCCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Qy	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780

Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCATTTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCATTTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGTTTATAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGTTTATAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCGAGGTT	1740

Db	1681	 CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAACTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAACTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640

Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTCAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTCAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGATTCTCAG	3240
Db	3181	GTCCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGATTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTT	3420
Qy	3421	CTTCTGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCTGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540

Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCTTGAGTACCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCTTGAGTACCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTAGTTCTC	3780
Db	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTAGTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTAC	4080
Qy	4081	CATCAACTTCACCTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACCTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440

Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400

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Db      5341  |||||TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTCTTCTCCATGCACTGAGCA 5400
Qy      5401  TCTGCTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
Db      5401  |||||TCTGCTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
Qy      5461  CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Db      5461  |||||CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Qy      5521  CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Db      5521  |||||CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Qy      5581  GTGGAGTGTCATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT 5640
Db      5581  |||||GTGGAGTGTCATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT 5640
Qy      5641  GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
Db      5641  |||||GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

```

RESULT 3

US-08-299-849B-8

; Sequence 8, Application US/08299849B

; Patent No. 5612201

; GENERAL INFORMATION:

; APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;

; APPLICANT: Leth , Bernard; Szikora, Jean-Pierre; De Smet, Charles;

; APPLICANT: Chomez, Patrick

; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In

; TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor

; NUMBER OF SEQUENCES: 48

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felte & Lynch

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; CITY: New York City

; STATE: New York

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/299,849B

; FILING DATE: 1-SEPTEMBER-1994

; CLASSIFICATION: 435

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; APPLICATION NUMBER: 08/037,230

; FILING DATE: 26-MARCH-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/04354

; FILING DATE: 22-MAY-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/807,043

; FILING DATE: 12-DECEMBER-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/764,364

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; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; APPLICATION NUMBER: 9-JULY-1991
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; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-May-1991
; ATTORNEY/AGENT INFORMATION:
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; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
US-08-299-849B-8

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Query Match          100.0%; Score 5674; DB 2; Length 5674;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
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Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTCTCAACCCAGGGAAGCCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

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Qy	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Db	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Qy	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCA	600
Db	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCA	600
Qy	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Db	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Qy	661	CACCCCCACCCCAACCCCAACGCCCACTCCACCCCAACCCAGGCAGGATCCGGTTCCCG	720
Db	661	CACCCCCACCCCAACCCCAACGCCCACTCCACCCCAACCCAGGCAGGATCCGGTTCCCG	720
Qy	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440

Db	1381	 GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCATTTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	 TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCATTTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	 ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCCAAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	 ACTGAGGAGGCACACACCCCAAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	 CCAGCCCTGGACCACCCGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	 CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	 GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	 ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861	 CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	 TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	 GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCTCAGAGGACCCAGCACCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	 TGCGAGATGAGGGAGGCTCAGAGGACCCAGCACCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	 ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	 GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	 GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340

Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAGGGGTAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAGGGGTAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCC TTGGTCTGAGAAGGCTGCGCTCAGGT CAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCC TTGGTCTGAGAAGGCTGCGCTCAGGT CAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCC TCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCC TCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAAC TCTTGATTTGGATTTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAAC TCTTGATTTGGATTTCTCAG	3240

Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCTCTCACTTCCT	3660
Qy	3661	CCTTCAGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140

QY	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCAC TAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCAC TAAGAAGGTGGC	4200
QY	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
QY	4261	AATGCTGGAGAGTGT CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGT CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
QY	4321	CTCTGAGTCCTTG CAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTG CAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
QY	4381	CTCCTATGTCTTGTCACCTGCCTAGGTCTCTCTATGATGGCTTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCTTGTCACCTGCCTAGGTCTCTCTATGATGGCTTGCTGGGTGATAATCA	4440
QY	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
QY	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
QY	4561	GGAGCACAGTGCCATG GGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCATG GGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
QY	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
QY	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
QY	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
QY	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGACTGGGCCAGTGCACCTT	4860
QY	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
QY	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
QY	4981	TATCTTTGTTCTCTTTTGAATGTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATGTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
QY	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100

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Db      5041  |||||TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAAGGG 5100
Qy      5101  TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT 5160
Db      5101  |||||TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT 5160
Qy      5161  AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA 5220
Db      5161  |||||AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA 5220
Qy      5221  AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA 5280
Db      5221  |||||AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA 5280
Qy      5281  ATTTTAAAGATATATGCATACCTGGATTTCTTGCTTATACCTCAGTCTATTCTGTAAA 5340
Db      5281  |||||ATTTTAAAGATATATGCATACCTGGATTTCTTGCTTATACCTCAGTCTATTCTGTAAA 5340
Qy      5341  TAAATCTGAATAAAGAATTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400
Db      5341  |||||TAAATCTGAATAAAGAATTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400
Qy      5401  TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
Db      5401  |||||TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
Qy      5461  CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Db      5461  |||||CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Qy      5521  CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Db      5521  |||||CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Qy      5581  GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCTTCT 5640
Db      5581  |||||GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCTTCT 5640
Qy      5641  GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
Db      5641  |||||GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

```

RESULT 4

US-08-560-024-1

; Sequence 1, Application US/08560024

; Patent No. 5843448

; GENERAL INFORMATION:

; APPLICANT: Chen, Yao-Tseng; Stockert, Elisabeth;

; APPLICANT: Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.;

; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry;

; APPLICANT: Old, Lloyd J.

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH BIND TO

; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSOR MAGE-1, RECOMBINANT MAGE-1

; TITLE OF INVENTION: AND MAGE-1 DERIVED IMMUNOGENIC PEPTIDES

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felte & Lynch

; STREET: 805 Third Avenue

; CITY: New York City

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; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,024
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 037,230
; FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; APPLICATION NUMBER: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5843448man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5354
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; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
US-08-560-024-1

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Query Match          100.0%;  Score 5674;  DB 2;  Length 5674;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 5674;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
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Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy      61 ATCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
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Db      61 ATCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

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Qy	121	CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG	180
Db	121	CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG	180
Qy	181	TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Db	181	TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Qy	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Db	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Qy	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Db	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Qy	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Db	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Qy	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Db	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Qy	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Db	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Qy	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Db	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Qy	601	CCCCACATCCCCACCCCATCCCTCAACCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Db	601	CCCCACATCCCCACCCCATCCCTCAACCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Qy	661	CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Db	661	CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Qy	721	CCAGGAAACATCCGGGTGCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721	CCAGGAAACATCCGGGTGCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080



Db	1021		TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081		GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081		GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141		CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTTCGCATTCCCATTCCCACCCAACC	1200
Db	1141		CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTTCGCATTCCCATTCCCACCCAACC	1200
Qy	1201		CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Db	1201		CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Qy	1261		ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCCTCACTGCCCCAAC	1320
Db	1261		ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCCTCACTGCCCCAAC	1320
Qy	1321		CCCACCCCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321		CCCACCCCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381		GGTTTGGCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381		GGTTTGGCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441		TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441		TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501		ATCCACTGAGGGGAGTGTTTATAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501		ATCCACTGAGGGGAGTGTTTATAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561		ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561		ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621		CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621		CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681		CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681		CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741		GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741		GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801		ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801		ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861		CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861		CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921		TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980

Db 1921 TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA 1980

Qy 1981 GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC 2040  
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Db 1981 GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC 2040

Qy 2041 TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG 2100  
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Db 2041 TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG 2100

Qy 2101 ACTGAGGCTGCCACTTCTGGCCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG 2160  
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Db 2101 ACTGAGGCTGCCACTTCTGGCCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG 2160

Qy 2161 GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT 2220  
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Db 2161 GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT 2220

Qy 2221 GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG 2280  
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Db 2221 GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG 2280

Qy 2281 GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC 2340  
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Db 2281 GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC 2340

Qy 2341 TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG 2400  
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Db 2341 TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG 2400

Qy 2401 AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT 2460  
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Db 2401 AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT 2460

Qy 2461 TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA 2520  
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Db 2461 TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA 2520

Qy 2521 CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT 2580  
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Db 2521 CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT 2580

Qy 2581 ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT 2640  
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Db 2581 ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT 2640

Qy 2641 GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAGGGGTCAGCCCTGGACACC 2700  
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Db 2641 GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAGGGGTCAGCCCTGGACACC 2700

Qy 2701 TCACCCAGGATGTGGCTTCTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT 2760  
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Db 2701 TCACCCAGGATGTGGCTTCTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT 2760

Qy 2761 CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG 2820  
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Db 2761 CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG 2820

Qy 2821 GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG 2880  
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Db 2821 GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG 2880

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Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTTCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTTCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTT	3420
Qy	3421	CTTCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
Db	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780

Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCATATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCATATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740

Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Qy	5221	AGAATAAAGAAATTAAGAGATAGTCAATTCTTGCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAATAAAGAAATTAAGAGATAGTCAATTCTTGCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Db	5401	TCTGCTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Qy	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Db	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Qy	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Db	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Qy	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCCTTCT	5640

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Db      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640

Qy      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
          |||||
Db      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

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RESULT 5

US-08-142-368A-8

; Sequence 8, Application US/08142368A

; Patent No. 5925729

; GENERAL INFORMATION:

```

; APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
; APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
; APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
; NUMBER OF SEQUENCES: 26

```

; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022

```

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect

```

; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/142,368A
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435

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; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992

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; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991

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; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991

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; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 07/728,838
; APPLICATION NUMBER: 9-JULY-1991

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; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-May-1991

```

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```

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; REFERENCE/DOCKET NUMBER: LUD 5253.4-US

```

; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884

```

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

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; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: genomic DNA  
; FEATURE:  
; NAME/KEY: MAGE-1 gene  
US-08-142-368A-8

Query Match 100.0%; Score 5674; DB 2; Length 5674;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
      |||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
      |||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
      |||
Db    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
      |||
Db    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
      |||
Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
      |||
Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
      |||
Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGGAGCGTCCAGGCTCTGCCAGACAT 480
      |||
Db    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGGAGCGTCCAGGCTCTGCCAGACAT 480

Qy    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540
      |||
Db    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540

Qy    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600
      |||
Db    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600

Qy    601 CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT 660
      |||
Db    601 CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT 660

Qy    661 CACCCCCACCCCAACCCCAAGCCCACTCCACCCCAACCCAGGCAGGATCCGGTTCCCG 720
      |||
Db    661 CACCCCCACCCCAACCCCAAGCCCACTCCACCCCAACCCAGGCAGGATCCGGTTCCCG 720

Qy    721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780
      |||
Db    721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780
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Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740



Db	1681		CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGCAGGGTT	1740
Qy	1741		GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCCGCATTAGGGTCAGG	1800
Db	1741		GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCCGCATTAGGGTCAGG	1800
Qy	1801		ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801		ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861		CCACTCACATTCCCATACCTACCCCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Db	1861		CCACTCACATTCCCATACCTACCCCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Qy	1921		TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCATCCA	1980
Db	1921		TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981		GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981		GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041		TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041		TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101		ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101		ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161		GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161		GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221		GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221		GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281		GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281		GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341		TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341		TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401		AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401		AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461		TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461		TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521		CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521		CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581		ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640

Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTGAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTGAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540

Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCTCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTCAATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTCAATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTGATAATCA	4440

Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTTCCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTTCCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTCTTCTCCATGCACTGAGCA	5400

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Db      5341  |||||TAAATCTGAATAAAGAATTCTTCTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400
Qy      5401  TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
Db      5401  |||||TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
Qy      5461  CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Db      5461  |||||CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Qy      5521  CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Db      5521  |||||CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Qy      5581  GTGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
Db      5581  |||||GTGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
Qy      5641  GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
Db      5641  |||||GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

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RESULT 6

US-08-967-727-8

; Sequence 8, Application US/08967727

; Patent No. 6025474

; GENERAL INFORMATION:

; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;

; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry

; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For

; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felte & Lynch

; STREET: 805 Third Avenue

; CITY: New York City

; STATE: New York

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/967,727

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/037,230

; FILING DATE: 26-MARCH-1993

; APPLICATION NUMBER: PCT/US92/04354

; FILING DATE: 22-MAY-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/807,043

; FILING DATE: 12-DECEMBER-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/764,365

; FILING DATE: 23-SEPTEMBER-1991

; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6025474man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
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; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
US-08-967-727-8

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Query Match          100.0%; Score 5674; DB 3; Length 5674;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCCGGGGCACCACCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
        |||
Db      1 CCCGGGGCACCACCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
        |||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
        |||
Db    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
        |||
Db    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
        |||
Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
        |||
Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
        |||
Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480
        |||
Db    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

Qy    481 CATGCTCAGGATTCTCAAGGAGGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540
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Db 481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCCTCCCGTGACCCAAC 540  
 Qy 541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600  
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 Db 541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600  
 Qy 601 CCCCACATCCCCCACCCTCAACCTGATGCCCATCCGCCAGCCATTCCACCCCT 660  
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 Db 601 CCCCACATCCCCCACCCTCAACCTGATGCCCATCCGCCAGCCATTCCACCCCT 660  
 Qy 661 CACCCCCACCCCCACCCCCACGCCACTCCCACCCCCACCCAGGCAGGATCCGGTTCCCG 720  
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 Db 661 CACCCCCACCCCCACCCCCACGCCACTCCCACCCCCACCCAGGCAGGATCCGGTTCCCG 720  
 Qy 721 CCAGGAAACATCCGGGTGCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 721 CCAGGAAACATCCGGGTGCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780  
 Qy 781 GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840  
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 Db 781 GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840  
 Qy 841 CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 841 CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA 900  
 Qy 901 GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA 960  
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 Db 901 GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA 960  
 Qy 961 CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC 1020  
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 Db 961 CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC 1020  
 Qy 1021 TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG 1080  
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 Db 1021 TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG 1080  
 Qy 1081 GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC 1140  
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 Db 1081 GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC 1140  
 Qy 1141 CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC 1200  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1141 CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC 1200  
 Qy 1201 CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC 1260  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1201 CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC 1260  
 Qy 1261 ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCCAAC 1320  
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 Db 1261 ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCCAAC 1320  
 Qy 1321 CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATTCCTGGCAGAATCC 1380  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1321 CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATTCCTGGCAGAATCC 1380  
 Qy 1381 GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT 1440  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1381 GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT 1440

Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCCAAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCCAAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCC TACCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCC TACCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCC TAGGACACCGACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCC TAGGACACCGACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340



Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTCAGCCC TGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTCAGCCC TGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCC TCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCC TCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAAC TTTGATTGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAAC TTTGATTGATTCTCAG	3240
Qy	3241	ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300

Db	3241	 ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCTTCCTG	3360
Db	3301	 CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCTTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTT	3420
Db	3361	 GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	 CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	 ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	 GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	 TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	 CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Db	3721	 GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Db	3781	 AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	 CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	 TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCTCTGCTCCTGGGCACCTTGAGGAGGTGCC	4020
Db	3961	 TGTGCAGGCTGCCACCTCCTCCTCTCTCTGCTCCTGGGCACCTTGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	 CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081'	 CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCTGAGTCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200

Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
QY	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
QY	4261	AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
QY	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
QY	4381	CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTGATAATCA	4440
QY	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
QY	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
QY	4561	GGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCAAGATTTGGTGCAGGAAAA	4620
QY	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
QY	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
QY	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
QY	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
QY	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
QY	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
QY	4981	TATCTTTGTTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
QY	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100

Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCCTGTTCAGTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCCTGTTCAGTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Db	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Qy	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Db	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Qy	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Db	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Qy	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTCTTGGGCTTTGGGAAACTGCAGTTCCTTCT	5640
Db	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTCTTGGGCTTTGGGAAACTGCAGTTCCTTCT	5640
Qy	5641	GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674
Db	5641	GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674

RESULT 7

US-08-037-230D-8

; Sequence 8, Application US/08037230D

; Patent No. 6235525

; GENERAL INFORMATION:

; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;

; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry

; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For

; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felte & Lynch

; STREET: 805 Third Avenue

; CITY: New York City

; STATE: New York

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

; COMPUTER: IBM

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;   OPERATING SYSTEM:  PC-DOS
;   SOFTWARE:  Wordperfect
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/037,230D
;   FILING DATE:  26-MARCH-1993
;   CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  PCT/US92/04354
;   FILING DATE:  22-MAY-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  07/807,043
;   FILING DATE:  12-DECEMBER-1991
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  07/764,364
;   FILING DATE:  23-SEPTEMBER-1991
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  07/728,838
;   FILING DATE:  9-JULY-1991
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  07/705,702
;   FILING DATE:  23-MAY-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Hanson, No. 6235525man D.
;   REGISTRATION NUMBER:  30,946
;   REFERENCE/DOCKET NUMBER:  LUD 5353
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (212) 688-9200
;   TELEFAX:  (212) 838-3884
;   INFORMATION FOR SEQ ID NO:  8:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  5674 base pairs
;   TYPE:  nucleic acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  genomic DNA
;   FEATURE:
;   NAME/KEY:  MAGE-1 gene
US-08-037-230D-8

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Query Match          100.0%;  Score 5674;  DB 3;  Length 5674;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 5674;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy      1  CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC  60

Qy     61  ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG  120

Qy    121  CTCTCAACCCAGGGAAGCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  CTCTCAACCCAGGGAAGCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG  180

Qy    181  TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG  240

Qy    241  CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC  300
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Db	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Qy	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Db	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Qy	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Db	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Qy	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Db	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Qy	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Db	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Qy	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Db	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Qy	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT	660
Db	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT	660
Qy	661	CACCCCCACCCCAACCCCAACCCCACTCCCAACCCCAACCCAGGCAGGATCCGGTTCCCG	720
Db	661	CACCCCCACCCCAACCCCAACCCCACTCCCAACCCCAACCCAGGCAGGATCCGGTTCCCG	720
Qy	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC	1200

Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCGTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCGTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCATTTAATGGTTCGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCATTTAATGGTTCGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100

Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTGAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTGAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCAGGCC	3060



Db	3001		ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061		CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCAGGACACATTAATTCCAAT	3120
Db	3061		CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCAGGACACATTAATTCCAAT	3120
Qy	3121		GAATTTTGATATCTCTTGCTGCCCCTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121		GAATTTTGATATCTCTTGCTGCCCCTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181		GTCCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGATTCTCAG	3240
Db	3181		GTCCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGATTCTCAG	3240
Qy	3241		ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241		ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301		CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301		CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361		GTAGACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTTCCT	3420
Db	3361		GTAGACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTTCCT	3420
Qy	3421		CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421		CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481		ACAGAGCAGAGGATGCACAGGGGTGCGCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481		ACAGAGCAGAGGATGCACAGGGGTGCGCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541		GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541		GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601		TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601		TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661		CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661		CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721		GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Db	3721		GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Qy	3781		AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Db	3781		AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Qy	3841		CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841		CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901		TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCTGGTGTG	3960

Db 3901 TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG 3960

Qy 3961 TGTGCAGGCTGCCACCTCCTCCTCCTCCTCCTGCTGCTGGGCACCTGGAGGAGGTGCC 4020  
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Db 3961 TGTGCAGGCTGCCACCTCCTCCTCCTCCTCCTGCTGCTGGGCACCTGGAGGAGGTGCC 4020

Qy 4021 CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC 4080  
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Db 4021 CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC 4080

Qy 4081 CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG 4140  
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Db 4081 CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG 4140

Qy 4141 GCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC 4200  
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Db 4141 GCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC 4200

Qy 4201 TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA 4260  
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Db 4201 TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA 4260

Qy 4261 AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC 4320  
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Db 4261 AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC 4320

Qy 4321 CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGCCA 4380  
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Db 4321 CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGCCA 4380

Qy 4381 CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTGATAATCA 4440  
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Db 4381 CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTGATAATCA 4440

Qy 4441 GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG 4500  
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Db 4441 GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG 4500

Qy 4501 CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG 4560  
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Db 4501 CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG 4560

Qy 4561 GGAGCACAGTGCCATGGGGAGCCCAGGAAGCTGCTCACCAAGATTTGGTGCAGGAAAA 4620  
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Db 4561 GGAGCACAGTGCCATGGGGAGCCCAGGAAGCTGCTCACCAAGATTTGGTGCAGGAAAA 4620

Qy 4621 GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT 4680  
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Db 4621 GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT 4680

Qy 4681 CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT 4740  
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Db 4681 CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT 4740

Qy 4741 GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG 4800  
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Db 4741 GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG 4800

Qy 4801 GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGACCTT 4860  
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Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
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Db	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTTGGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAAC	5460
Db	5401	TCTGCTTTTTGGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAAC	5460
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Db	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Qy	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT	5640
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Db	5641	GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674

RESULT 8

US-09-583-850-8

; Sequence 8, Application US/09583850

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; Patent No. 6498021
; GENERAL INFORMATION:
; APPLICANT: Gaugler, Batrice; Van den Eynde, BenoEt;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/583,850
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/583,613
; FILING DATE:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,365
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6498021man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
US-09-583-850-8

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Query Match          100.0%;  Score 5674;  DB 3;  Length 5674;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 5674;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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 Db 781 GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840

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Db	961	 CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	 TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	 GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
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Db	1201	 CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCCCTCACTGCCCCAAC	1320
Db	1261	 ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCCCTCACTGCCCCAAC	1320
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Db	1321	 CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
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Db	1381	 GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	 TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	 ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
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Db	1561	 ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
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Db	1621	 CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	 CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCGGCATTAGGGTCAGG	1800
Db	1741	 GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860

Db 1801 ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC 1860

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Db 1861 CCACTCACATTCCCATACCTACCCCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG 1920

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Db 1921 TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA 1980

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Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
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Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
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Qy 4561 GGAGCACAGTGCCATGGGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA 4620

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Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
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Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
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Qy	4981	TATCTTTGTTCTCTTTTGAATGTGTTCAAATGTTTTTTTTTAAGGGATGGTGAATGAAC	5040
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Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Db	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Qy	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520

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Db      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Qy      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Qy      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
Qy      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
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Db      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

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RESULT 9

US-09-579-197-8

; Sequence 8, Application US/09579197

; Patent No. 6552180

; GENERAL INFORMATION:

; APPLICANT: Gaugler, Beatrice; Van den Eynde, Benoit;

; van der Bruggen, Pierre; Boon-Falleur, Thierry

; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding

; For Tumor Rejection Antigen Precursor Mage-3 And Uses The

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch

; STREET: 805 Third Avenue

; CITY: New York City

; STATE: New York

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/579,197

; FILING DATE: 26-May-2000

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/037,230

; FILING DATE:

; APPLICATION NUMBER: 07/807,043

; FILING DATE: 12-DECEMBER-1991

; APPLICATION NUMBER: 07/764,364

; FILING DATE: 23-SEPTEMBER-1991

; APPLICATION NUMBER: 07/728,838

; FILING DATE: 9-JULY-1991

; APPLICATION NUMBER: 07/705,702

; FILING DATE: 23-MAY-1991

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; REFERENCE/DOCKET NUMBER: LUD 5353

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; TELEPHONE: (212) 688-9200

; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5674 base pairs

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;          TYPE: nucleic acid
;          STRANDEDNESS: single
;          TOPOLOGY: linear
;          MOLECULE TYPE: genomic DNA
;          FEATURE:
;          . NAME/KEY:  MAGE-1 gene
;          SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-579-197-8

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Query Match          100.0%;  Score 5674;  DB 3;  Length 5674;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 5674;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
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Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
        |||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
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Db    121 CTCTCAACCCAGGGAAGCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
        |||
Db    181 TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
        |||
Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
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Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
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Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480
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Db    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

Qy    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCCTGACCCAAAC 540
        |||
Db    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCCTGACCCAAAC 540

Qy    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600
        |||
Db    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600

Qy    601 CCCCACATCCCCCACCCTCAACCCCTGATGCCATCCGCCAGCCATTCCACCCCT 660
        |||
Db    601 CCCCACATCCCCCACCCTCAACCCCTGATGCCATCCGCCAGCCATTCCACCCCT 660

Qy    661 CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCTCG 720
        |||
Db    661 CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCTCG 720

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Qy 721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780  
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 Db 721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780

Qy 781 GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840  
 |||  
 Db 781 GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840

Qy 841 CTCGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA 900  
 |||  
 Db 841 CTCGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA 900

Qy 901 GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA 960  
 |||  
 Db 901 GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA 960

Qy 961 CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC 1020  
 |||  
 Db 961 CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC 1020

Qy 1021 TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG 1080  
 |||  
 Db 1021 TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG 1080

Qy 1081 GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC 1140  
 |||  
 Db 1081 GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC 1140

Qy 1141 CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC 1200  
 |||  
 Db 1141 CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC 1200

Qy 1201 CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTACCTGACCACC 1260  
 |||  
 Db 1201 CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTACCTGACCACC 1260

Qy 1261 ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCAAC 1320  
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 Db 1261 ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCAAC 1320

Qy 1321 CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC 1380  
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 Db 1321 CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC 1380

Qy 1381 GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT 1440  
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 Db 1381 GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT 1440

Qy 1441 TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG 1500  
 |||  
 Db 1441 TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG 1500

Qy 1501 ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG 1560  
 |||  
 Db 1501 ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG 1560

Qy 1561 ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG 1620  
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 Db 1561 ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG 1620

Qy 1621 CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC 1680

Db	1621		1680
Qy	1681	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1740
Db	1681		1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741		1800
Qy	1801	ACCCTGGGAGGGAAGTGGAGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801		1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Db	1861		1920
Qy	1921	TCAACCACGGAAGCCACGGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCATCCA	1980
Db	1921		1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981		2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041		2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101		2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161		2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221		2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281		2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341		2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401		2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461		2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580

Db 2521 CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT 2580

Qy 2581 ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT 2640  
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Db 2581 ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT 2640

Qy 2641 GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTCAGCCCTGGACACC 2700  
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Db 2641 GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTCAGCCCTGGACACC 2700

Qy 2701 TCACCCAGGATGTGGCTTCTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT 2760  
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Db 2701 TCACCCAGGATGTGGCTTCTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT 2760

Qy 2761 CATTCTCAGAGGGTGAAGTCAAGTACAGGACCCCATCTGGTCTAAAGACAGAGCG 2820  
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Db 2761 CATTCTCAGAGGGTGAAGTCAAGTACAGGACCCCATCTGGTCTAAAGACAGAGCG 2820

Qy 2821 GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG 2880  
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Db 2821 GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG 2880

Qy 2881 GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCAGAG 2940  
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Db 2881 GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCAGAG 2940

Qy 2941 AGCATGGGCTGGGCCGCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG 3000  
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Db 2941 AGCATGGGCTGGGCCGCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG 3000

Qy 3001 ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC 3060  
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Db 3001 ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC 3060

Qy 3061 CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCAGGACACATTAATTCCAAT 3120  
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Db 3061 CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCAGGACACATTAATTCCAAT 3120

Qy 3121 GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT 3180  
 |||

Db 3121 GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT 3180

Qy 3181 GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG 3240  
 |||

Db 3181 GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG 3240

Qy 3241 ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA 3300  
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Db 3241 ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA 3300

Qy 3301 CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCACCCCTCCTG 3360  
 |||

Db 3301 CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCACCCCTCCTG 3360

Qy 3361 GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGATTCTCT 3420  
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Db 3361 GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGATTCTCT 3420

Qy 3421 CTTCTGAGCTCCAGGAACAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC 3480  
 |||

Db 3421 CTTCTGAGCTCCAGGAACAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC 3480

Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCCTCCTCTGGTCTTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCCTCCTCCTCTGGTCTTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTCAATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTCAATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380



Qy 4381 CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA 4440  
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 Db 4381 CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA 4440

Qy 4441 GATCATGCCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG 4500  
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 Db 4441 GATCATGCCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG 4500

Qy 4501 CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG 4560  
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Qy 4561 GGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA 4620  
 |||  
 Db 4561 GGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA 4620

Qy 4621 GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT 4680  
 |||  
 Db 4621 GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT 4680

Qy 4681 CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT 4740  
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Qy 4741 GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG 4800  
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 Db 4741 GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG 4800

Qy 4801 GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT 4860  
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 Db 4801 GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT 4860

Qy 4861 CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT 4920  
 |||  
 Db 4861 CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT 4920

Qy 4921 GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT 4980  
 |||  
 Db 4921 GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT 4980

Qy 4981 TATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC 5040  
 |||  
 Db 4981 TATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC 5040

Qy 5041 TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG 5100  
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 Db 5041 TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG 5100

Qy 5101 TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT 5160  
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 Db 5101 TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT 5160

Qy 5161 AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA 5220  
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 Db 5161 AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA 5220

Qy 5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA 5280  
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 Db 5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA 5280

Qy 5281 ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT 5340

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Db      5281  |||||||||||||||||||||||||||||||||||||||||||||||||||||| 5340
Qy      5341  TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400
Db      5341  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5341  TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400
Qy      5401  TCTGCTTTTTTGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
Db      5401  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5401  TCTGCTTTTTTGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
Qy      5461  CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Db      5461  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5461  CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Qy      5521  CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Db      5521  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5521  CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Qy      5581  GTGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCTTCT 5640
Db      5581  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5581  GTGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCTTCT 5640
Qy      5641  GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
Db      5641  ||||||||||||||||||||||||||||||||||
Db      5641  GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

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RESULT 10
US-09-404-026-8
; Sequence 8, Application US/09404026
; Patent No. 6565857
; GENERAL INFORMATION:
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/404,026
; FILING DATE: 23-SEPT-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/037,230
; FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043

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; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6565857man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
US-09-404-026-8

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Query Match          100.0%; Score 5674; DB 3; Length 5674;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
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Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
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Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
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Db    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

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Db    181 TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

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Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
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Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
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Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

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Qy	481		CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCCTCCCGTGACCCAAC	540
Db	481		CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCCTCCCGTGACCCAAC	540
Qy	541		CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCCCTCTTCATTGTCATTCCAACCCCCA	600
Db	541		CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCCCTCTTCATTGTCATTCCAACCCCCA	600
Qy	601		CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCCAGCCATTCCACCCCT	660
Db	601		CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCCAGCCATTCCACCCCT	660
Qy	661		CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Db	661		CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Qy	721		CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721		CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781		GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781		GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841		CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Db	841		CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Qy	901		GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901		GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961		CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Db	961		CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Qy	1021		TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021		TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081		GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081		GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141		CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATCCCCACCCAACC	1200
Db	1141		CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATCCCCACCCAACC	1200
Qy	1201		CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Db	1201		CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Qy	1261		ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261		ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321		CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380

Db 1321 CCCACCCATCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATTTCTGGCAGAATCC 1380

Qy 1381 GGT TTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT 1440  
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Db 1381 GGT TTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT 1440

Qy 1441 TGAACCTCACAGATCTGAGAGAAGCCAGGTTCAATTAATGGTTCTGAGGGGCGGCTTGAG 1500  
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Db 1441 TGAACCTCACAGATCTGAGAGAAGCCAGGTTCAATTAATGGTTCTGAGGGGCGGCTTGAG 1500

Qy 1501 ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG 1560  
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Db 1501 ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG 1560

Qy 1561 ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG 1620  
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Db 1561 ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG 1620

Qy 1621 CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCCGTCCCGTCC 1680  
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Db 1621 CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCCGTCCCGTCC 1680

Qy 1681 CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT 1740  
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Db 1681 CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT 1740

Qy 1741 GGTCAGGAGAGGCAGGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG 1800  
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Db 1741 GGTCAGGAGAGGCAGGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG 1800

Qy 1801 ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC 1860  
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Db 1801 ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC 1860

Qy 1861 CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG 1920  
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Db 1861 CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG 1920

Qy 1921 TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA 1980  
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Db 1921 TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA 1980

Qy 1981 GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC 2040  
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Db 1981 GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC 2040

Qy 2041 TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG 2100  
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Db 2041 TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG 2100

Qy 2101 ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG 2160  
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Db 2101 ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG 2160

Qy 2161 GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT 2220  
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Db 2161 GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT 2220

Qy 2221 GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG 2280  
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Db 2221 GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG 2280

Qy	2281	GCCCATATTTCTGTCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGTCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAGGGGTCAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAGGGGTCAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
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Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCAGGCC	3060
Db	3001	ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180

Qy	3181	GTCCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGATTGTTCTCAG	3240
Db	3181	GTCCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGATTGTTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCCTGAGGGCCCGTGATTCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCCTGAGGGCCCGTGATTCT	3420
Qy	3421	CTTCTGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCTCAGGTC	3480
Db	3421	CTTCTGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCTGAGTACCTCTCACTTCT	3660
Db	3601	TCAGTCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCTGAGTACCTCTCACTTCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTAGTTCTC	3780
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Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCCTTCCCCTACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCCTTCCCCTACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140

Db	4081		CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141		GCCAAGCACCTCTTGTATCCTGGAGTCCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141		GCCAAGCACCTCTTGTATCCTGGAGTCCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201		TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201		TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261		AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261		AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321		CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321		CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381		CTCCTATGTCTTGTTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381		CTCCTATGTCTTGTTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441		GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441		GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501		CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501		CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561		GGAGCACAGTGCCATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561		GGAGCACAGTGCCATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621		GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621		GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681		CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681		CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741		GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741		GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801		GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801		GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861		CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Db	4861		CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Qy	4921		GAAGAGAGCGGTCAGTGTTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921		GAAGAGAGCGGTCAGTGTTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981		TATCTTTGTTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040





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; STATE: New York
; COUNTRY:
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312,464
; FILING DATE: 17-May-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/967,727
; FILING DATE: 27-NOVEMBER-1997
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-May-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6599699man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5253.5-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)318-3168
; TELEFAX: (212)752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-312-464-8

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Query Match          100.0%;  Score 5674;  DB 3;  Length 5674;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 5674;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
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Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
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Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
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Db    121 CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

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Qy	181	TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGC TTGAGATCGGTGGAGGGAAGCGGG	240
Db	181	TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGC TTGAGATCGGTGGAGGGAAGCGGG	240
Qy	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Db	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Qy	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Db	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Qy	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Db	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Qy	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Db	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Qy	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Db	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Qy	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Db	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Qy	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Db	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Qy	661	CACCCCCACCCCAACCCCAACGCCCCACTCCACCCCAACCCAGGCAGGATCCGGTTCCCG	720
Db	661	CACCCCCACCCCAACCCCAACGCCCCACTCCACCCCAACCCAGGCAGGATCCGGTTCCCG	720
Qy	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080

Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040

Db	1981	 GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	 TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	 ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	 GTGGGACCCAGGCCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	 GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	 GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	 TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCCTT	2460
Db	2401	 AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	 TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	 CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	 ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTCAGCCCTGGACACC	2700
Db	2641	 GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTCAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	 TCACCCAGGATGTGGCTTCTTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	 CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	 GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTACCCAGAG	2940

Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTCACCCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTC	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTC	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAATTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAATTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840

Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTCAATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTCAATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740

Qy	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTTAAAGATATATGCATACCTGGATTTCCCTTGCCCTTTGAGAATGTAAGAGAAAAT	5340
Db	5281	ATTTTTTAAAGATATATGCATACCTGGATTTCCCTTGCCCTTTGAGAATGTAAGAGAAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Db	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Qy	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Db	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Qy	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Db	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Qy	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCCTTCT	5640
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Qy	5641	GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674



|||||  
Db 5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

RESULT 12

US-09-583-848A-8

; Sequence 8, Application US/09583848A

; Patent No. 6946289

; GENERAL INFORMATION:

; APPLICANT: Gaugler, Beatrice; Van den Eynde, Benoit; van der Bruggen,  
; Pierre; Boon-Falleur, Thierry

; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For Tumor  
; Rejection Antigen Precursor Mage-3 And Uses Thereof

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

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; CITY: New York City

; STATE: New York

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; ZIP: 10103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/583,848A

; FILING DATE: 31-May-2000

; CLASSIFICATION: 435

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; FILING DATE: 22-MAY-1992

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; APPLICATION NUMBER: 07/764,364

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; APPLICATION NUMBER: 07/728,838

; FILING DATE: 9-JULY-1991

; APPLICATION NUMBER: 07/705,702

; FILING DATE: 23-MAY-1991

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; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5674 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: genomic DNA

; FEATURE:

; NAME/KEY: MAGE-1 gene

; SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-09-583-848A-8

Query Match 100.0%; Score 5674; DB 3; Length 5674;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
      |||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
      |||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
      |||
Db    121 CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
      |||
Db    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
      |||
Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
      |||
Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCAC'TGGGGACTCGAAGTCAGAG 420
      |||
Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCAC'TGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480
      |||
Db    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

Qy    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540
      |||
Db    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540

Qy    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600
      |||
Db    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600

Qy    601 CCCCACATCCCCACCCCATCCCTCAACCTGATGCCATCCGCCAGCCATTCCACCCT 660
      |||
Db    601 CCCCACATCCCCACCCCATCCCTCAACCTGATGCCATCCGCCAGCCATTCCACCCT 660

Qy    661 CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG 720
      |||
Db    661 CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG 720

Qy    721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780
      |||
Db    721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780

Qy    781 GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840
      |||
Db    781 GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840

Qy    841 CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA 900
      |||
```

Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATCTTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATCTTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800

Qy	1801	ACCCTGGGAGGGAAC TGAGGGT TCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAAC TGAGGGT TCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAGGGGTGAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAGGGGTGAGCCCTGGACACC	2700

Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGAAGTCAAGTACAGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGAAGTCAAGTACAGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTTCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTTCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCACCCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCACCCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTTCCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTTCCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660

Db	3601	 TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	 CCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Db	3721	 GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Db	3781	 AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Qy	3841	CCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	 CCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	 TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	 TGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	 CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	 CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	 GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	 TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	 AATGCTGGAGAGTGTATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	 CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	 CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	 GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560

Db 4501 CCATGCTCCTGAGGAGGAAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG 4560

Qy 4561 GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAA 4620  
 |||

Db 4561 GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAA 4620

Qy 4621 GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT 4680  
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Db 4621 GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT 4680

Qy 4681 CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT 4740  
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Db 4681 CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT 4740

Qy 4741 GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG 4800  
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Db 4741 GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG 4800

Qy 4801 GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT 4860  
 |||

Db 4801 GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT 4860

Qy 4861 CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCTACTCT 4920  
 |||

Db 4861 CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCTACTCT 4920

Qy 4921 GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT 4980  
 |||

Db 4921 GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT 4980

Qy 4981 TATCTTTGTTCTCTTTTGAATGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC 5040  
 |||

Db 4981 TATCTTTGTTCTCTTTTGAATGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC 5040

Qy 5041 TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG 5100  
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Db 5041 TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG 5100

Qy 5101 TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT 5160  
 |||

Db 5101 TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT 5160

Qy 5161 AACAGCAGTGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA 5220  
 |||

Db 5161 AACAGCAGTGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA 5220

Qy 5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA 5280  
 |||

Db 5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA 5280

Qy 5281 ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT 5340  
 |||

Db 5281 ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT 5340

Qy 5341 TAAATCTGAATAAAGAATTCTTCCGTTCAGTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400  
 |||

Db 5341 TAAATCTGAATAAAGAATTCTTCCGTTCAGTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400

Qy 5401 TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAC 5460  
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Db 5401 TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAC 5460

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Qy      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
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Db      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520

Qy      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
        |||
Db      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580

Qy      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
        |||
Db      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640

Qy      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
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Db      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

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# RESULT 13

US-09-949-016-12445

; Sequence 12445, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 12445

; LENGTH: 5699

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-12445

Query Match 69.3%; Score 3934.8; DB 3; Length 5699;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 4002; Conservative 0; Mismatches 2; Indels 6; Gaps 6;

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Qy      1669 CCCGTCCCGTCCCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGAC 1728
        |||
Db      1 CCCGTCCCGTCCCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGAC 60

Qy      1729 CGGGGCAGGGTTGGTCAGGAGA-GGCAGGGCCAGGCATCAAGGTCCA-GCATCCGCCCCG 1786
        |||
Db      61 CGGGGCAGGGTTGGTCAGGAGAGGGCAGGGCCAGGCATCAAGGTCCAGGCATCCGCCCCG 120

Qy      1787 GCATTAGGGTCAGGACCCTGGGAGGGAAGTGAAGGTTCCCCACCCACACCTGTCTCCTCA 1846
        |||
Db      121 GCATTAGGGTCAGGACCCTGGGAGGGAAGTGAAGGTTCCCCACCCACACCTGTCTCCTCA 180

Qy      1847 TCTCCACCGCCACCCCACTCACATTCCCATACTACCCCTACCCCCAACCTCATCTTGT 1906
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Db 181 TCTCCACCGCCACCCCACTCACATTTCCATACCTACCCCTACCCCCAACCTCATCTTGT 240  
 Qy 1907 CAGAATCCCTGCTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTT 1966  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 CAGAATCCCTGCTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTT 300  
 Qy 1967 GACGTCCCCATCCAGGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAG 2026  
 |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||  
 Db 301 GACGTCCCCATCCAGGG-CTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAG 359  
 Qy 2027 AGGGAGGGCCCCTACTGCGAGATGAGGGAGGCC TCAGAGGACCCAGCACCCCTAGGACACCG 2086  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 360 AGGGAGGGCCCCTACTGCGAGATGAGGGAGGCC TCAGAGGACCCAGCACCCCTAGGACACCG 419  
 Qy 2087 CACCCCTGTCTGAGACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACT 2146  
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 Db 420 CACCCCTGTCTGAGACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAAATGATGGGGACT 479  
 Qy 2147 CAGATT-GCATGGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAG 2205  
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 Db 480 CAGATTAGCATGGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAG 539  
 Qy 2206 GACTCAGGGGACCTTGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCA 2265  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 540 GACTCAGGGGACCTTGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCA 599  
 Qy 2266 CGGTGGCCACATATGGCCCATATTTCTGTCATCTTTGAGGTGACAGGACAGAGCTGTGGT 2325  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 600 CGGTGGCCACATATGGCCCATATTTCTGTCATCTTTGAGGTGACAGGACAGAGCTGTGGT 659  
 Qy 2326 CTGAGAAGTGGGGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGA 2385  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 660 CTGAGAAGTGGGGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGA 719  
 Qy 2386 TGTGCCCCCTTCATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAG 2445  
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 Db 720 TGTGCCCCCTTCATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAG 779  
 Qy 2446 TCTGGCTGTCCCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCA 2505  
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 Db 780 TCTGGCTGTCCCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCA 839  
 Qy 2506 TTCTCACTTGTACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGT 2565  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 840 TTCTCACTTGTACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGT 899  
 Qy 2566 AAAGGGGGGATGTCTACTCATGTACAGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCA 2625  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 900 AAAGGGGGGATGTCTACTCATGTACAGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCA 959  
 Qy 2626 GGAATAAAGATGAGTGAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAAGGGG 2685  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 960 GGAATAAAGATGAGTGAGACAGACAAGGCTATTGGAATCCTCACCCAGAACCAAAGGGG 1019  
 Qy 2686 TCAGCCCTGGACACCTCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGG 2745  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1020 TCAGCCCTGGACACCTCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGG 1078  
 Qy 2746 GGCAGGTGAGGACCTCATTTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGG 2805  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1079 GGCAGGTGAGGACCTCATTTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGG 1138

Qy	2806	TCTAAAGACAGAGCGGTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGA	2865
Db	1139	TCTAAAGACAGAGCGGTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGA	1198
Qy	2866	CTGAGGGTACCCCAGGACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCCT	2925
Db	1199	CTGAGGGTACCCCAGGACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCCT	1258
Qy	2926	GCTGTCACCCCAGAGAGCATGGGCTGGGCCGTCTGCCGAGGTCCCTCCGTTATCCTGGGA	2985
Db	1259	GCTGTCACCCCAGAGAGCATGGGCTGGGCCGTCTGCCGAGGTCCCTCCGTTATCCTGGGA	1318
Qy	2986	TCATTGATGTCAGGGACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAG	3045
Db	1319	TCATTGATGTCAGGGACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAG	1378
Qy	3046	GGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGA	3105
Db	1379	GGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGA	1438
Qy	3106	CACATTAATTCCAATGAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACG	3165
Db	1439	CACATTAATTCCAATGAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACG	1498
Qy	3166	TGTGGCCAGATGTTTGTCCCCCTCCTGTCCTTCCATTCTTATCATGGATGTGAACCTTTG	3225
Db	1499	TGTGGCCAGATGTTTGTCCCCCTCCTGTCCTTCCATTCTTATCATGGATGTGAACCTTTG	1558
Qy	3226	ATTTGGATTTCTCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAG	3285
Db	1559	ATTTGGATTTCTCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAG	1618
Qy	3286	GGCCCTGCGTGAGAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTC	3345
Db	1619	GGCCCTGCGTGAGAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTC	1678
Qy	3346	CAGCCCACCCTCCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAG	3405
Db	1679	CAGCCCACCCTCCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAG	1738
Qy	3406	GGCCCGTGGATTCTCTTCTTCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGA	3465
Db	1739	GGCCCGTGGATTCTCTTCTTCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGA	1798
Qy	3466	CAGTATCCTCAGGTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCC	3525
Db	1799	CAGTATCCTCAGGTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCC	1858
Qy	3526	CTGAATGCACACCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGC	3585
Db	1859	CTGAATGCACACCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGC	1918
Qy	3586	CTCACCTCCCTACTGTCAGTCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGT	3645
Db	1919	CTCACCTCCCTACTGTCAGTCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGT	1978
Qy	3646	ACCCTCTCACTTCCTCCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCC	3705
Db	1979	ACCCTCTCACTTCCTCCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCC	2038

Qy	3706	CTGGAGGCCACAGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCCTTGTAGAGTCTC	3765
Db	2039	CTGGAGGCCACAGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCCTTGTAGAGTCTC	2098
Qy	3766	CAAGGTTTCAGTTCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCAGGCCTGTGGGT	3825
Db	2099	CAAGGTTTCAGTTCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCAGGCCTGTGGGT	2158
Qy	3826	CTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTC	3885
Db	2159	CTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTC	2218
Qy	3886	TCTTGAGCAGAGGAGTCTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGC	3945
Db	2219	TCTTGAGCAGAGGAGTCTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGC	2278
Qy	3946	CCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCTGGGCAC	4005
Db	2279	CCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCCTCTGGTCTGGGCAC	2338
Qy	4006	CCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTC	4065
Db	2339	CCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTC	2398
Qy	4066	CGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAG	4125
Db	2399	CGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAG	2458
Qy	4126	CCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAAT	4185
Db	2459	CCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAAT	2518
Qy	4186	CACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCC	4245
Db	2519	CACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCC	2578
Qy	4246	AGTCACAAAGGCAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGA	4305
Db	2579	AGTCACAAAGGCAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGA	2638
Qy	4306	GATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGC	4365
Db	2639	GATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGC	2698
Qy	4366	AGACCCACCGGCCACTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCT	4425
Db	2699	AGACCCACCGGCCACTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCT	2758
Qy	4426	GCTGGGTGATAATCAGATCATGCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGAT	4485
Db	2759	GCTGGGTGATAATCAGATCATGCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGAT	2818
Qy	4486	TGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGA	4545
Db	2819	TGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGA	2878
Qy	4546	GGTGTATGATGGGAGGGAGCACAGTGCCATGGGGAGCCCAGGAAGCTGCTCACCCAAGA	4605
Db	2879	GGTGTATGATGGGAGGGAGCACAGTGCCATGGGGAGCCCAGGAAGCTGCTCACCCAAGA	2938
Qy	4606	TTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTA	4664

Db	2939	TTTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCACGCTA	2998
Qy	4665	TGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTA	4724
Db	2999	TGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTA	3058
Qy	4725	TGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTT	4784
Db	3059	TGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTT	3118
Qy	4785	GAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGAC	4844
Db	3119	GAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGAC	3178
Qy	4845	TGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAG	4904
Db	3179	TGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAG	3238
Qy	4905	GCCCATTCTTCACTCTGAAGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATT	4964
Db	3239	GCCCATTCTTCACTCTGAAGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATT	3298
Qy	4965	GGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGAATTGTTCAAATGTTTTTTTTTAAG	5024
Db	3299	GGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGAATTGTTCAAATGTTTTTTTTTAAG	3358
Qy	5025	GGATGGTTGAATGAACCTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGT	5084
Db	3359	GGATGGTTGAATGAACCTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGT	3418
Qy	5085	GTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTAGATTGGGAAATCCATTCTATTT	5144
Db	3419	GTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTAGATTGGGAAATCCATTCTATTT	3478
Qy	5145	TGTGAATTGGGATAATAACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGT	5204
Db	3479	TGTGAATTGGGATAATAACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGT	3538
Qy	5205	AAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCT	5264
Db	3539	AAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCT	3598
Qy	5265	CAGTCTATTCTGTAAATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTG	5324
Db	3599	CAGTCTATTCTGTAAATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTG	3658
Qy	5325	AGAATGTAAGAGAAATTAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTT	5384
Db	3659	AGAATGTAAGAGAAATTAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTT	3718
Qy	5385	CTCCATGCACTGAGCATCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGG	5444
Db	3719	CTCCATGCACTGAGCATCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGG	3778
Qy	5445	TAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATC	5504
Db	3779	TAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATC	3838
Qy	5505	GAGGTGGCAAGATGTCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGG	5564

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Db      3839 GAGGTGGCAAGATGTCCTCTAAAGATGTAGGAAAAGTGAGAGAGGGGTGAGGGTGTGGG 3898
Qy      5565 GCTCCGGGTGAGAGTGGTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGA 5624
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3899 GCTCCGGGTGAGAGTGGTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGA 3958
Qy      5625 AACTGCAGTTCCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3959 AACTGCAGTTCCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 4008

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RESULT 14

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US-09-949-016-14430
; Sequence 14430, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14430
; LENGTH: 5699
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14430

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Query Match          69.3%; Score 3934.8; DB 3; Length 5699;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4002; Conservative 0; Mismatches 2; Indels 6; Gaps 6;

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Qy      1669 CCCGTCCCGTCCCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGAC 1728
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Db      1   CCCGTCCCGTCCCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGAC 60
Qy      1729 CGGGGCAGGGTTGGTCAGGAGA-GGCAGGGCCCAGGCATCAAGGTCCA-GCATCCGCCCCG 1786
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61   CGGGGCAGGGTTGGTCAGGAGAGGGCAGGGCCCAGGCATCAAGGTCCAGGCATCCGCCCCG 120
Qy      1787 GCATTAGGGTCAGGACCTGGGAGGGAAGTGGAGGGTTCCCCACCCACACCTGTCTCCTCA 1846
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GCATTAGGGTCAGGACCTGGGAGGGAAGTGGAGGGTTCCCCACCCACACCTGTCTCCTCA 180
Qy      1847 TCTCCACCGCCACCCCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGT 1906
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TCTCCACCGCCACCCCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGT 240
Qy      1907 CAGAATCCCTGCTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTT 1966
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CAGAATCCCTGCTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTT 300
Qy      1967 GACGTCCCCATCCAGGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAG 2026

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Db	301	 GACGTCCCCATCCAGGG-CTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAG	359
Qy	2027	AGGGAGGGCCCTACTGCGAGATGAGGGAGGGCTCAGAGGACCCAGCACCCCTAGGACACCG	2086
Db	360	 AGGGAGGGCCCTACTGCGAGATGAGGGAGGGCTCAGAGGACCCAGCACCCCTAGGACACCG	419
Qy	2087	CACCCCTGTCTGAGACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACT	2146
Db	420	 CACCCCTGTCTGAGACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAAATGATGGGGACT	479
Qy	2147	CAGATT-GCATGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAG	2205
Db	480	 CAGATTAGCATGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAG	539
Qy	2206	GACTCAGGGGACCTTGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCA	2265
Db	540	 GACTCAGGGGACCTTGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCA	599
Qy	2266	CGGTGGCCACATATGGCCCATATTTCTGTCATCTTTGAGGTGACAGGACAGAGCTGTGGT	2325
Db	600	 CGGTGGCCACATATGGCCCATATTTCTGTCATCTTTGAGGTGACAGGACAGAGCTGTGGT	659
Qy	2326	CTGAGAAGTGGGGCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGA	2385
Db	660	 CTGAGAAGTGGGGCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGA	719
Qy	2386	TGTGCCCCCTTCATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAG	2445
Db	720	 TGTGCCCCCTTCATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAG	779
Qy	2446	TCTGGCTGTCCCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCA	2505
Db	780	 TCTGGCTGTCCCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCA	839
Qy	2506	TTCTCACTTGTACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGT	2565
Db	840	 TTCTCACTTGTACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGT	899
Qy	2566	AAAGGGGGGATGTCTACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCA	2625
Db	900	 AAAGGGGGGATGTCTACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCA	959
Qy	2626	GGAATAAAGATGAGTGAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAAGGGG	2685
Db	960	 GGAATAAAGATGAGTGAGACAGACAAGGCTATTGGAATCCTCACCCAGAACCAAAGGGG	1019
Qy	2686	TCAGCCCTGGACACCTCACCCAGGATGTGGCTTCTTTTCTACTCCTGTTTCCAGATCTGG	2745
Db	1020	 TCAGCCCTGGACACCTCACCCAGGATGTGGCTTC-TTTTCTACTCCTGTTTCCAGATCTGG	1078
Qy	2746	GGCAGGTGAGGACCTCATTCTCAGAGGGTGAAGTCAACGTAGGGACCCCATCTGG	2805
Db	1079	 GGCAGGTGAGGACCTCATTCTCAGAGGGTGAAGTCAACGTAGGGACCCCATCTGG	1138
Qy	2806	TCTAAAGACAGAGCGGTCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGA	2865
Db	1139	 TCTAAAGACAGAGCGGTCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGA	1198
Qy	2866	CTGAGGGTACCCAGGACCAGAACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCT	2925

Db	1199	CTGAGGGTACCCCAGGACCAGAACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCCT	1258
Qy	2926	GCTGTCACCCCAGAGAGCATGGGCTGGGCCGTCTGCCGAGGTCC TTCCGTTATCCTGGGA	2985
Db	1259	GCTGTCACCCCAGAGAGCATGGGCTGGGCCGTCTGCCGAGGTCC TTCCGTTATCCTGGGA	1318
Qy	2986	TCATTGATGTCAGGGACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAG	3045
Db	1319	TCATTGATGTCAGGGACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAG	1378
Qy	3046	GGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGA	3105
Db	1379	GGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGA	1438
Qy	3106	CACATTAATTCCAATGAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACG	3165
Db	1439	CACATTAATTCCAATGAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACG	1498
Qy	3166	TGTGGCCAGATGTTTGTCCCTCCTGTCCTTCCATTCTTATCATGGATGTGAACTCTTG	3225
Db	1499	TGTGGCCAGATGTTTGTCCCTCCTGTCCTTCCATTCTTATCATGGATGTGAACTCTTG	1558
Qy	3226	ATTTGGATTTCTCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAG	3285
Db	1559	ATTTGGATTTCTCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAG	1618
Qy	3286	GGCCCTGCGTGAGAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTC	3345
Db	1619	GGCCCTGCGTGAGAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTC	1678
Qy	3346	CAGCCCACCTCCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCTTGAG	3405
Db	1679	CAGCCCACCTCCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCTTGAG	1738
Qy	3406	GGCCCGTGGATTCTCTTCTTCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGA	3465
Db	1739	GGCCCGTGGATTCTCTTCTTCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGA	1798
Qy	3466	CAGTATCCTCAGGTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCC	3525
Db	1799	CAGTATCCTCAGGTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCC	1858
Qy	3526	CTGAATGCACACCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGC	3585
Db	1859	CTGAATGCACACCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGC	1918
Qy	3586	CTCACCTCCCTACTGTCAGTCTCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGT	3645
Db	1919	CTCACCTCCCTACTGTCAGTCTCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGT	1978
Qy	3646	ACCTCTCACTTCCTCCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGACAGGATTCC	3705
Db	1979	ACCTCTCACTTCCTCCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGACAGGATTCC	2038
Qy	3706	CTGGAGGCCACAGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTC	3765
Db	2039	CTGGAGGCCACAGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTC	2098
Qy	3766	CAAGGTTTCAGTTCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGT	3825
Db	2099	CAAGGTTTCAGTTCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGT	2158

Qy	3826	CTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTC	3885
Db	2159	CTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTC	2218
Qy	3886	TCTTGAGCAGAGGAGTCTGCAAGCCTGAGGAAGCCCTTGAGGCCAACAAAGAGGC	3945
Db	2219	TCTTGAGCAGAGGAGTCTGCAAGCCTGAGGAAGCCCTTGAGGCCAACAAAGAGGC	2278
Qy	3946	CCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCCTCTGGTCTGGGCAC	4005
Db	2279	CCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCCTCTGGTCTGGGCAC	2338
Qy	4006	CCTGGAGGAGGTGCCCACCTGCTGGGTCAACAGATCCTCCCCAGAGTCTCAGGGAGCCTC	4065
Db	2339	CCTGGAGGAGGTGCCCACCTGCTGGGTCAACAGATCCTCCCCAGAGTCTCAGGGAGCCTC	2398
Qy	4066	CGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAG	4125
Db	2399	CGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAG	2458
Qy	4126	CCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAAT	4185
Db	2459	CCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAAT	2518
Qy	4186	CACTAAGAAGGTGGCTGATTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCC	4245
Db	2519	CACTAAGAAGGTGGCTGATTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCC	2578
Qy	4246	AGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTCTGA	4305
Db	2579	AGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTCTGA	2638
Qy	4306	GATCTTCGGCAAAGCCTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGC	4365
Db	2639	GATCTTCGGCAAAGCCTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGC	2698
Qy	4366	AGACCCACCGGCCACTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCT	4425
Db	2699	AGACCCACCGGCCACTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCT	2758
Qy	4426	GCTGGGTGATAATCAGATCATGCCAAGACAGGCTTCTGATAATTGTCTGGTCATGAT	4485
Db	2759	GCTGGGTGATAATCAGATCATGCCAAGACAGGCTTCTGATAATTGTCTGGTCATGAT	2818
Qy	4486	TGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGA	4545
Db	2819	TGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGA	2878
Qy	4546	GGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGA	4605
Db	2879	GGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGA	2938
Qy	4606	TTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTA	4664
Db	2939	TTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCACGCTA	2998
Qy	4665	TGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTA	4724
Db	2999	TGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTA	3058



Qy	4725	TGTGATCAAGGTCAGTGCAAGAGTTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTT	4784
Db	3059	TGTGATCAAGGTCAGTGCAAGAGTTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTT	3118
Qy	4785	GAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGAC	4844
Db	3119	GAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGAC	3178
Qy	4845	TGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCTGCGTCGTGTGACATGAG	4904
Db	3179	TGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCTGCGTCGTGTGACATGAG	3238
Qy	4905	CCCCATTCTTCACTCTGAAGAGAGCGGTCAAGTGTCTCAGTAGTAGGTTTCTGTTCTATT	4964
Db	3239	CCCCATTCTTCACTCTGAAGAGAGCGGTCAAGTGTCTCAGTAGTAGGTTTCTGTTCTATT	3298
Qy	4965	GGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGAATGTTCAAATGTTTTTTTTTAAG	5024
Db	3299	GGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGAATGTTCAAATGTTTTTTTTTAAG	3358
Qy	5025	GGATGGTTGAATGAACCTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGT	5084
Db	3359	GGATGGTTGAATGAACCTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGT	3418
Qy	5085	GTATATAGTTTAAAGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTT	5144
Db	3419	GTATATAGTTTAAAGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTT	3478
Qy	5145	TGTGAATTGGGATAATAACAGCAGTGAATAAGTACTTAGAAATGTGAAAAATGAGCAGT	5204
Db	3479	TGTGAATTGGGATAATAACAGCAGTGAATAAGTACTTAGAAATGTGAAAAATGAGCAGT	3538
Qy	5205	AAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCT	5264
Db	3539	AAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCT	3598
Qy	5265	CAGTCTATTCTGTAAAATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTG	5324
Db	3599	CAGTCTATTCTGTAAAATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTG	3658
Qy	5325	AGAATGTAAGAGAAATTAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTT	5384
Db	3659	AGAATGTAAGAGAAATTAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTT	3718
Qy	5385	CTCCATGCACCTGAGCATCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGG	5444
Db	3719	CTCCATGCACCTGAGCATCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGG	3778
Qy	5445	TAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATC	5504
Db	3779	TAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATC	3838
Qy	5505	GAGGTGGCAAGATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGG	5564
Db	3839	GAGGTGGCAAGATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGG	3898
Qy	5565	GCTCCGGGTGAGAGTGGTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGA	5624
Db	3899	GCTCCGGGTGAGAGTGGTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGA	3958
Qy	5625	AACTGCAGTTCCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674

Db 3959 AACTGCAGTTCCCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 4008

Query Match 46.8%; Score 2655; DB 3; Length 11495;  
Best Local Similarity 73.6%; Pred. No. 0;  
Matches 4231; Conservative 0; Mismatches 1100; Indels 416; Gaps 50;

Qy	487	CAGGATTCTCAAGGAGAGGGCTGAGGGTCCCTTAAGACCCCACTCCCGTGACCCAACCCCCAC	546
Db	6437		
		CAGGACCCTAGGAGAGGGCTGAGTGTCCCCA---CCCCATTCTATCCCCTACCCCTT	6493
Qy	547	TCCAATGCTCACTCCCGTGACCAACCCCTCTTCATTGTCAATTCCAACCCCCACCCAC	606
Db	6494		
		TCCCATCTGCACTCCC-----TACCCATCTGTACCCCC	6527
Qy	607	ATCCCCACCCCATCCCTCAACCCGTGATGCCCATCCGCCAGCCATTCCACCCTCACCCC	666
Db	6528		
		ATTCCCCACCTGTGCCCCCTATCTCCCCAACCCCCCAACCAGCCTCATACCCCCCTCCCC	6587
Qy	667	CACCCCCACCCCAACGCCCACTCCCACCCCAACCAGGCAGGATCCG-GTTCCCGCCAGG	725
Db	6588		
		CACCCCTACCTTCATCCCCATCAGTGCAGCATCCGGTTCCACCCCTGCTTTCAATCCAGG	6647
Qy	726	AAACATCCGGGTGCCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGAGAAGC	785
Db	6648		
		CAAGCCCTGGGTGGCCGGATGTGATGCCACTGACTTGTGAATTGAGGGTTAGAGAGAAGT	6707
Qy	786	GAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGGCTCTG	845
Db	6708		
		GAGTTTCTGGGTCTGAAGGGTGGC-TTGAGATCGGCAGAGGGAAGGTGGCCAGGCTTTG	6766
Qy	846	TGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATAGAGAG	905
Db	6767		
		TGAAGAGGCAAAGTGAGACTCTGAGGGAGGATTCAGGAAACCCCTATCCCTGATAGAGGG	6826
Qy	906	CCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGACGTCT	965
Db	6827		
		TCCCAGCCCTGGACTACCC-----CGCGGAGGCTGACTTCT	6862
Qy	966	CAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTCTTCTC	1025
Db	6863		
		CAGACTGGGCTGCTCCCCACCTCCGCCCC-----TTCGCAACGCGTTTGTTTAAGCCAC	6917
Qy	1026	CCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGGGCAGG	1085
Db	6918		
		AGGGGACTCTGGAGTCAGAGGTTGGTGTGATCAGGGAAGGGCTGGTTAGGAGA-GGCATG	6976
Qy	1086	GCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCCCCAAG	1145
Db	6977		
		GCCCAGGCCCTGCCAGGAATCAAAGTCAGAAACC-TGAGAGGGAAC TGAGTCCCCCAAG	7035
Qy	1146	ACTGCACTCCAATCCCCACTCCCACCCATTCGCATTCCCATTCCCCACCCAACCCCCAT	1205
Db	7036		
		ATCCTAGTCTAACCCCCACTCCACAA-----	7062
Qy	1206	CTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTACCTGACCACCACCCCT	1265
Db	7063		
		-----ATCCGCTGCCATTTCGCTGCTCCATTTCCTATCTTGCCT	7104
Qy	1266	CCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCCCTCACTGCCCCCAACCCAC	1325
Db	7105		
		CCACCCTACCA-----	7116
Qy	1326	CCTCATCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATCTGGCAGAATCCGGTTT	1385
Db	7117		
		-----GGCAGAATCCAGTTC	7133

Qy	1386	GCC-CCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAACCACTGACTTGAA	1444
Db	7132	CCCTTCTGCTATCAATCCAGGGAACCCAGGCTTGGTGCTGGGATGTTTTT-----	7183
Qy	1445	CCTCACAGATCTGAGAGAAGCCAGGTTCAATTAATGGTTCTGAGGGGCGGCTTGAGATCC	1504
Db	7184	-----TGGGGGTCAGAGAATCAAGGGCATAGTCCTGAGGGGCCAGTTGAGATCG	7232
Qy	1505	ACTGAGGGGAGTGGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGGACTG	1564
Db	7233	GCTGAGGGGAGCGGGCCCAAGCTCTGTGGCGAGGCAAGGTGAGACTCTGAGGAAGGACTG	7292
Qy	1565	AGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTGCCAG	1624
Db	7293	AGGAGGCCCCCAACCAAGATAGA-GGAACCCAAATAATCCAGCGCAGCTCCTGCTGCCAG	7351
Qy	1625	CCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCGTCCTGTCCTCCACT	1684
Db	7352	TCTTGGACCACCCGG---GGGAAGACTTCTCA---GGCTAGGCCATCCAGCTCCTCCACT	7404
Qy	1685	GCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTTGGTC	1744
Db	7405	GCCACTAAAGCTACAGGGGACTCTAGAGTCAAGAGCTTGGTGTGCCCA-----	7452
Qy	1745	AGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGGACCC	1804
Db	7453	-----AGGCAGGGCCAGGC-----TCTGCCTGGCATCGGGGTCAGGACCT	7493
Qy	1805	TGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACCCAC	1864
Db	7494	TGAGAGGGAAC TGAGGGCGCTACACCCCAACCCATCCGCATTC-----CAACAT	7543
Qy	1865	TCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTGTCAA	1924
Db	7544	GCCCAGCCCCATCCCCAAGTCCGTTTGCAGAATCCATTTT---TCCCTGCAGTCAA	7599
Qy	1925	CCCACGGAAGCCACGGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCATCCAGGGT	1984
Db	7600	CCCCGGAAGACCTGGGAATGGT---CAGGCACCTCGGATCTTGACATCCACATCGAGGGC	7656
Qy	1985	CTGATGGAGGGAAGGGG-----CTTGAACAGGGCCTCAGGGGAGCAGAGGGAG-----	2032
Db	7657	TGAAGGAGGGAGAGGGTTTGGTATCATGAGCAGAGCCTCAGGGTAGCAGAGGGAGGACCC	7716
Qy	2033	-GGCCCTACTGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCC-----TAGGAC	2082
Db	7717	TGGCCCTCCTGGGAGATGAGGAAGGCCTCAGGAGACCCAGCACCCCAAGGCAGGGAGCCC	7776
Qy	2083	ACCGCACCCCTGTCTGAGACTGAG--GCTGCCACTTCTGGCCTCAAGAATCAGAACGATG	2140
Db	7777	ACCCACCCCTGTCTGAGAATGAGGTGCCTCCTCTTTTAGCCTCAGGAATCCAAGGGATG	7836
Qy	2141	GGGACTCAGATTGCAT--GGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAG	2198
Db	7837	GCAACTCAGGTCAGCAGAGGGGTGGGTCCAAGCCCTTCCAGGATCAAGGAAAGGAAGAC	7896
Qy	2199	GAGGGAGGACTCAGGGGACCTTGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTC	2258
Db	7897	GAGGGAGGATTCAGGGGGCCTTGCAATCCAGATCAGTGGAGACCTGGGCCCTGGGAGGTC	7956
Qy	2259	CAGGGCACGGTGGCCACATATGGCCCATATTTCTGCATCTTTGAGGT----GACAGGAC	2311

Db	7957	CTGGGGCAAGGTAGCCACCTGTAGCTCATACTTCCTGCATCTTCGAGGTCACAGAGAGGAG	8016
Qy	2315	AGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCAT	2374
Db	8017	AGGGCTATGGTCTGAGGGGTGGTACTTCAGGTCCGCAGAGGGAGGAGTCCCAGGATCTAC	8076
Qy	2375	ATGGCCCAAGATGTGCC-CCCTTCATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGG	2433
Db	8077	AGGACCCAAGGTGTGCCACACTTCACGAGGAATGGGGATACCTGTGGCTCAGAAAGACGG	8136
Qy	2434	GACTCCACACAGTCTGGCTGTCCCCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGG	2493
Db	8137	GACCCACAGAGTCTGGCTGTCCCCTGTTCTTAGCTCAGGGGGGACCAGAGGAGGGATGG	8196
Qy	2494	CGGTATGTTCCATTCTCACTTGTACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATG	2553
Db	8197	CCCTATGTGCCAATTCACCTTGTTCACAGGCAGGAAGTTGGGGAACCTTCAGGGAGATG	8256
Qy	2554	GGGTCTTGGGGTAAAGGGGGGATGTCTACTCATGTCAGGGAATTGGGGGTTGAGGAAGCA	2613
Db	8257	AGGTTTTGGAGTAAAGGGGCAATGTTTGCTCATCTCAGGGGGTTGGGGGTTGAGGAAGGG	8316
Qy	2614	CAGGCGCTGGCAGGAATAAAGATGAGTGAGACAGACAAGGCTATTGGAATCCACACCCCA	2673
Db	8317	CAGGCCCTGTCAGGAGCAAACATGAGT-ACCCACAGGAGGCCATCAGAACCCTCACCCCA	8375
Qy	2674	GAACCAAAGGGGTCAGCCCTGGACACCTCACCCAG-----GATGTGGCTTCTTTTTTC	2725
Db	8376	GAACCAAAGGGGTCAGCCCTGGGCACCCACACAGGGGTGACAGGATGTGGCTCCTTCTC	8435
Qy	2726	ACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCTCATTCTCAGAGGGTGA CT CAGGTCA	2785
Db	8436	ATTTCTGATTCCAGATCTCAGTGAGGTGAGGACCTTGTTCTCAGAGGGTGA CT CAGGTCA	8495
Qy	2786	ACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCGGTCCCAGGATCTGCCATGCGTTCGG	2845
Db	8496	CCACAGGGACCCCCATCTGGTCTACAGACACAGTGGTCCCAGGATCTGCCAAGAGTCCTG	8555
Qy	2846	GTGAGGAACATGAGGGAGGACTGAGGGTACCCAGGACCAGAACACTGAGGGAGACTGCA	2905
Db	8556	GTGAGGAATGTGAGGGAGGATTGAGGGTACCACAGGGCCAGAACGCAGATGATGACCCCA	8615
Qy	2906	CAGAAATCAGCCCTGCCCCTGCTGTACCCCAGAGAGCATGGGCTGGGCCGTCTGCCGAG	2965
Db	8616	CAGAAATCAGCCCTGCTCCTGTTGTACCCCAGAGAGCATGGGCTTGGCTTTCTGCTGAG	8675
Qy	2966	GTCCTTCCGTTATCCTGGGATCATTGATGTGAGGGACGGGGAGGCCCTTGGTCTGAGAAGG	3025
Db	8676	GTCCCTCTCTTATCCTGGGATCACTGGTGTACGGAGTGGGAGGCCCTTGGTCTGAGGGGG	8735
Qy	3026	CTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACCA	3085
Db	8736	CTGCACCCAGGTCAGTAGAGGGAGGGTCCCAGGCTCTGCCAGGAGTTGAGGTGAGGACCA	8795
Qy	3086	AGCGGGCACCTCACCCAGGACACATTAATTCCAATGAATTTGATATCTCTTGCTGCCCT	3145
Db	8796	AGCAGGCTCCGCATCCAGGACACATGGGTTCGAATTCGACATCTTTTGCTGTCTGT	8855
Qy	3146	TC-CCCAAGGACCTAGGCACGTGTGGCCAGATGTTTGTCCCTCCTGTCTTCCATTCTCT	3204

Db		8856 TCTTCGGAAGACCTAGGCACAGGTGGCCAGATGTGGGGTTTCTTAGGTCCT---GTTCCC	8912
Qy	3205	TATCATGGATGTGA ACTCTTGATT TGATTTC TCAGACCAGCAAAAGGGCAGGATCCAGG 	3264
Db	8913	TCTCAGGCATGTGAGCTCTTGATCTGAGTTTC CAGGCCAGCAAAAGAGTGGGATCCAGG	8972
Qy	3265	CCCTGCCAGGAAAAAATAAGGGCCCTGCGTGAGA ACAGAGGGGGTCATCCACTGCATGA 	3324
Db	8973	CCCTGCC TGGAGAAATGTGAGGGCC CTGAGTGAACACAGTGGGGATCATCCACTCCATGA	9032
Qy	3325	GAGTGGGGATGT CACAGAGTCCAGCCCCCTCTCGGTAGCACTGAGAAGCCAGGGCTGT 	3384
Db	9033	GAGTGGGGACCTCACAGAGTCCAG CCTACCTCTTGATGGCACTGAGGGACCGGGGCTGT	9092
Qy	3385	GCTTGCGGTCTGC ACCCTGAGGGCC CGTGGATTCTCTTCCTGGAGCTCCAGGAACCAGG 	3444
Db	9093	GCTTACAGTCTGC ACCCTAAGGGCC CATGGATTCTCTCTCTAGGAGCTCCAGGAACAAGG	9152
Qy	3445	CAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATGCACAGGGTG 	3504
Db	9153	CAGTGAGGCCTTGGTCTGAGACAGTGTCTCAGGTTACAGAGCAGAGGATGCACAGGCTG	9212
Qy	3505	TGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAAGGGCCCCACCTGCCACAGGACACA 	3564
Db	9213	TGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAAGGGCCCCACCTGCCACAAGACACA	9272
Qy	3565	TAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCA GTCTCTGTAGAATCGACCTCTG 	3624
Db	9273	TAGGACTCCA AAGAGTCTGGCCTCACCTCCCTACCATCAATCCTGCAGAATCGACCTCTG	9332
Qy	3625	CTGGCCGGCTGTACCCTGA-GTACCCTCTCACTTCCTCCTTCAGGTTTTCAGGGGACAGG 	3683
Db	9333	CTGGCCGGCTATACCCTGAGGTGCTCTCACTTCCTCCTTCAGGTTCTGAGCAGACAGG	9392
Qy	3684	CCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAAGATCTGTA 	3743
Db	9393	CCAACCG - GAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAAGATCTGTA	9451
Qy	3744	AGTAGGCCTTTGTTAGAGTCTCCAAGG TTCAGTTCTCAGCTGAGGCCTCTCACACTCC 	3803
Db	9452	AGTAAGCCTTTGTTAGAGCCTCTAAGATTTGGTTCTCAGCTGAGGTCTCTCACATGCTCC	9511
Qy	3804	CTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCTGCCTGCTG 	3863
Db	9512	CTCTCTCCGTAGGCCTGTGGGTCCCCATTGCCCAGCTTTTGCTGCCTCTTGCTGCTG	9571
Qy	3864	CCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAG 	3923
Db	9572	CCCTGACCAGAGTCATCATGTCTTCTGAGCAGAAGAGTCAGCACTGCAAGCCTGAGGAAG	9631
Qy	3924	CCCTTGAGGCCCAACAAGAGGCCCTGGGCTGGTGTGTGTGCAGGCTGCCAC----- 	3975
Db	9632	GCGTTGAGGCCCAAGAAGAGGCCCTGGGCTGGTGGGTGCACAGGCTCCTACTACTGAGG	9691
Qy	3976	-----CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGC 	4019
Db	9692	AGCAGGAGGCTGCTGTCTCCTCCTCCTCTCCTCTGGTCCTGGCACCCTGGAGGAAGTGC	9751
Qy	4020	CCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTA 	4079
Db	9752	CTGCTGCTGAGTCAGCAGGTCCTCCCCAGAGTCCTCAGGGAGCCTCTGCCTTACCCACTA	9811

Qy	4080	CCATCAACTTTCACCTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGG	4139
Db	9812	CCATCAGCTTCACTTGTCTGGAGGCAACCCAATGAGGGTTCCAGCAGCCAAGAAGAGGAGG	9871
Qy	4140	GGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGG	4199
Db	9872	GGCCAAGCACCTCGCCTGACGCAGAGTCCTTGTTCGAGAAGCACTCAGTAACAAGGTGG	9931
Qy	4200	CTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAG	4259
Db	9932	ATGAGTTGGCTCATTTTTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCACAAAGGCAG	9991
Qy	4260	AAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAG	4319
Db	9992	AAATGCTGGAGAGAGTGTTCATCAAAAATTACAAGCGCTGTTTCTTGATCTTCGGCAAAG	10051
Qy	4320	CCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCC	4379
Db	10052	CCTCCGAGTCCCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCGCCAGCA	10111
Qy	4380	ACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATC	4439
Db	10112	ACACCTACACCCTTGTACCTGCCTGGGCCTTTCCCTATGATGGCCTGCTGGGTAATAATC	10171
Qy	4440	AGATCATGCCCAAGACAGGCTTCTTGATAATTGTCTGGTCATGATTGCAATGGAGGGCG	4499
Db	10172	AGATCTTTCCCAAGACAGGCCTTCTGATAATCGTCTGGGCACAATTGCAATGGAGGGCG	10231
Qy	4500	GCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGA	4559
Db	10232	ACAGCGCCTCTGAGGAGGAAATCTGGGAGGAGCTGGGTGTGATGGGGGTGTATGATGGGA	10291
Qy	4560	GGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAA	4619
Db	10292	GGGAGCACACTGTCTATGGGGAGCCCAGGAACTGCTCACCCAAGATTGGGTGCAGGAAA	10351
Qy	4620	AGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGG	4678
Db	10352	ACTACCTGGAGTACCGGCAGGTACCCGGCAGTAATCCTGCGCGCTATGAGTTCCTGTGGG	10411
Qy	4679	GTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCA	4738
Db	10412	GTCCAAGGGCTCTGGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGGTCAGGGTCA	10471
Qy	4739	GTGCAAGAGTTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAG	4798
Db	10472	ATGCAAGAGTTTCGATTGCCTACCCATCCCTGCGTGAAGCAGCTTTGTTAGAGGAGGAAG	10531
Qy	4799	AGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGG-----GGACTGGGCCAGTG	4854
Db	10532	AGGGAGTCTGAGCATGAGTTGCAGCCAGGGCTGTGGGGAAGGGGCAGGGCTGGGCCAGTG	10591
Qy	4855	CACCTTCCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTT	4914
Db	10592	CATCTAACA--GCCCTGTGCAGCAGCTTCCCTTGCTCGTGTAAACATGAGGCCATTCTT	10649
Qy	4915	CACTC----TGAAGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGA	4970
Db	10650	CACTCTGTTTGAAGAAAATAGTCAGTGTTCTTAGTAGTGGGTTTCTATTTTGTGTGGATGA	10709

Qy	4971	CTTGGAGATTATCTTTGTTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGG	5030
Db	10710	CTTGGAGATTATCTCTGTTTCCTTTTACAATTGTTGAAATG-TTCCTTTTAATGGATGG	10768
Qy	5031	TTGAATGAACCTTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATAT	5090
Db	10769	TTGAATTAACCTTCAGCATCCAAGTTTATGAATCGTAGTTAACGTATATTGCTGTTAATAT	10828
Qy	5091	AGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTGTGAA	5150
Db	10829	AGTTTAGGAGTAAGAGTCTTGTTTTTTATTTCAGATTGGGAAATCCGTTCTATTTGTGAA	10888
Qy	5151	TTGGG---ATAATAACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAA	5207
Db	10889	TTTGGGACATAATAACAGCAGTGGAGTAAGTATTTAGAAGTGTG---AATTCACCGTGAA	10945
Qy	5208	ATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAG	5267
Db	10946	ATAGGTGAGAT-----AAATTAAGATACTTAATTCCCGCCTTATGCCTCAG	10993
Qy	5268	TCTATTCTGTAAAATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGA	5327
Db	10994	TCTATTCTGTAAAATTTAAAAATATATATGCATACCTGGATTTCCTTGGCTTC---GTGA	11050
Qy	5328	ATGTAAGAGAAATTAAATCTGAATAAAGAATTCTTCTGTTCCTACTGGCTCTTTTCTTCTC	5387
Db	11051	ATGTAAGAGAAATTAAATCTGAATAAATAATTCTTTCTGTAACTGGCTCATTTCTTCTC	11110
Qy	5388	CATGCACTGAGCATCTGCTTTTTTGAAGGCCCTGGGTAGTAGTGGAGATGCTAAGGTAA	5447
Db	11111	TATGCACTGAGCATCTGCTCTGTGGAAGGCCAGGATTAGTAGTGGAGATACAGGGTAA	11170
Qy	5448	GCCAGACTCATACCCACCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAG	5507
Db	11171	GCCAGACACACACTACCGATAGGGTATTAAGAGTCTAGGAGCGCGGTCATATAATTAAAG	11230
Qy	5508	GTGGCAAGATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCT	5567
Db	11231	GTGACAAGATGTCCTCTAAGATGTAGGGGAAAAGT----AACGAGTGTGGGTATGGGGCT	11286
Qy	5568	CCGGGTGAGAGTGGTGGAGTGCAATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAAAC	5627
Db	11287	CCAGGTGAGAGTGGTGGGTGTAAATCCCTGTG-TGGGGCCTTTTGGGCTTTGGGAAAC	11345
Qy	5628	TGCAGTTCCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674
Db	11346	TGCATTTTCTTCTGAGGGATCTGATTCTAATGAAGCTTGGTGGGTCC	11392

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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2006, 10:02:12 ; Search time 24214 Seconds  
(without alignments)  
13103.423 Million cell updates/sec

Title: US-08-819-669E-8  
Perfect score: 5674  
Sequence: 1 CCCGGGGCACCCTGGCATC.....TAATGATCTGGGTGGATCC 5674

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_htc:\*  
7: gb\_est2:\*  
8: gb\_est7:\*  
9: gb\_est8:\*  
10: gb\_est9:\*  
11: gb\_gss1:\*  
12: gb\_gss2:\*  
13: gb\_gss3:\*  
14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	1062	18.7	1652	6	CR594285	CR594285 full-leng	
2	1036.4	18.3	2151	6	HSM806642	BX640600 Homo sapi	
3	1034.4	18.2	1671	6	CR622709	CR622709 full-leng	
4	1032	18.2	1689	6	CR595748	CR595748 full-leng	
5	1022.4	18.0	1738	6	CR623041	CR623041 full-leng	
6	1008.6	17.8	1661	6	CR611124	CR611124 full-leng	
7	918	16.2	930	14	DQ034885	DQ034885 Homo sapi	
8	840.2	14.8	1020	2	BM459064	BM459064 AGENCOURT	
9	787.2	13.9	923	14	DQ034886	DQ034886 Pan trogl	
10	783.6	13.8	1739	6	CR619399	CR619399 full-leng	
11	740.2	13.0	909	3	BU157186	BU157186 AGENCOURT	
c 12	720.2	12.7	747	4	CA428506	CA428506 UI-H-FE1-	
13	700	12.3	954	14	DQ049942	DQ049942 Homo sapi	
14	678.4	12.0	1008	14	DQ034795	DQ034795 Homo sapi	
15	675.8	11.9	811	3	BQ224380	BQ224380 AGENCOURT	
16	652	11.5	937	3	BU153093	BU153093 AGENCOURT	
c 17	645	11.4	668	4	CA423766	CA423766 UI-H-FE1-	
18	621.4	11.0	623	8	CV023387	CV023387 311 Full	
c 19	615.8	10.9	1044	1	AL562721	AL562721 AL562721	
c 20	615	10.8	637	3	BM989182	BM989182 UI-H-DP0-	
21	609	10.7	1191	3	BM907822	BM907822 AGENCOURT	
c 22	607.6	10.7	1041	4	BX361005	BX361005 BX361005	
23	602.6	10.6	957	14	DQ035556	DQ035556 Pan trogl	
24	601	10.6	957	14	DQ035555	DQ035555 Homo sapi	
25	583.8	10.3	918	14	DQ049943	DQ049943 Pan trogl	
26	583	10.3	964	4	BX361006	BX361006 BX361006	
27	566.6	10.0	922	3	BU175213	BU175213 AGENCOURT	
28	562.4	9.9	947	4	BX384326	BX384326 BX384326	
29	558.8	9.8	1006	14	DQ034796	DQ034796 Pan trogl	
30	537.4	9.5	876	2	BF792356	BF792356 602252896	
31	536.8	9.5	1021	2	BM470991	BM470991 AGENCOURT	
32	532.2	9.4	960	14	DQ031722	DQ031722 Pan trogl	
33	531	9.4	878	2	BG397171	BG397171 602434130	
34	528.8	9.3	960	14	DQ031721	DQ031721 Homo sapi	
35	526.6	9.3	1050	2	BG024106	BG024106 602303163	
36	525.2	9.3	1016	3	BM556490	BM556490 AGENCOURT	
37	524.6	9.2	1057	3	BM562570	BM562570 AGENCOURT	
38	524.4	9.2	1049	4	CA488474	CA488474 AGENCOURT	
39	523	9.2	1002	3	BM562465	BM562465 AGENCOURT	
40	522.6	9.2	802	14	DQ034776	DQ034776 Homo sapi	
41	522.6	9.2	962	2	BG116297	BG116297 602318570	
42	522.4	9.2	1011	4	BX341218	BX341218 BX341218	
43	520.8	9.2	872	2	BM449726	BM449726 AGENCOURT	
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#### ALIGNMENTS

RESULT 1  
CR594285  
LOCUS

CR594285

1652 bp

mRNA

linear

HTC 21-JUL-2004



Db	342	TCAGGGAGCCTCCACCTCCCCACTACCATCAACTATACTCTCTGGAGTCAATCCGATGA	401
Qy	4114	GGGTTCACGAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCCTTGT	4173
Db	402	GGGCTCCAGCAACGAAGAACAGGAAGGGCCAAGCACCTTTCCTGACCTGGAGACGAGCTT	461
Qy	4174	CCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCG	4233
Db	462	CCAAGTAGCACTCAGTAGGAAGATGGCTGAGTTGGTTTCATTTCTGCTCCTCAAGTATCG	521
Qy	4234	AGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCA	4293
Db	522	AGCCAGGGAGCCATTACAAAGGCAGAAATGCTGGGGAGTGTATCAGAAATTTCCAGGA	581
Qy	4294	CTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGA	4353
Db	582	CTTCTTTCTGTGATCTTCAGCAAAGCCTCCGAGTACTTGCAGCTGGTCTTTGGCATCGA	641
Qy	4354	CGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCTTGTACCTGCCTAGGTCTCTC	4413
Db	642	GGTGGTGGAAAGTGGTCCGCATCGGCCACTTGTACATCCTTGTACCTGCCTGGGCCTCTC	701
Qy	4414	CTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGT	4473
Db	702	CTACGATGGCTGCTGGGCGACAATCAGATCGTGCCCAAGACAGGCTTCCTGATAATCGT	761
Qy	4474	CCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCT	4533
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Qy	4534	GAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCAGGAAGCT	4593
Db	822	GAGTGTGTTGGAGGCATCTGATGGGAGGGAGGACAGTGTCTTTGCGCATCCAGGAAGCT	881
Qy	4594	GCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGA	4652
Db	882	GCTCACCCAAGATTTGGTGCAGGAAAAC TACCTGGAGTACCGCAGGTCCCCGGCAGTGA	941
Qy	4653	TCCCGCACGCTATGAGTTCCTGTGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAA	4712
Db	942	TCCTGCATGCTACGAGTTCTGTGGGTCCAAGGGCCCTCGTTGAAACCAGCTATGTGAA	1001
Qy	4713	AGTCCTTGAGTATGTGATCAAGGTCAAGTTCAGTTCGCTTTTTCTTCCCATCCCTGCG	4772
Db	1002	AGTCCTGCACCATTGCTAAAGATCAGTGGAGGACCTCACATTTCTACCCACCCCTGCA	1061
Qy	4773	TGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAG	4832
Db	1062	TGAATGGGCTTTTAGAGAGGGGAAGAGTGAGTCTGAGCACGAGTTGCAGCCAGGGCCAG	1121
Qy	4833	TGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCTGCCTC	4892
Db	1122	TGGGAGGGGGTCTGGGCCAGTGCACCTTCCAAGGCCCCATCCATTAGTTTCCACTGCCTC	1181
Qy	4893	GTGTGACATGAGGCCATTCTTCACTC--TGAAGAGAGCGGTGAGTGTCTCAGTAGTAG	4950
Db	1182	GTGTGATATGAGGCCATTCTTCACTCTTTGAAGAGAGCAGTCAGTATTGTTAGTAGTGA	1241
Qy	4951	GTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGGAATTGTTCAAA	5010
Db	1242	GTTTCTGTTCTATTGGATGACTTTGAGATTTATCTTTGTTTCTGTTGGAATTGTTCAAA	1301

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Qy      5011 TGT TTT TTT TTT TTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTTTATGAATGACAGCAG 5070
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Db      1302 TGTTC- TTTTAACGGATGGTTGAATGAACTTCAGCATCCAAGTTTATGAATGACAGTAG 1360

Qy      5071 TCACAC--AGTTCGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGG 5128
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Db      1361 TCACACATAGTGCTGTTTATATAGTTTAGGAGTAAGAGTGTGTTTTATTTCAGATTGG 1420

Qy      5129 GAAATCCATTCTATTTTGTGAATTGGGA-TAATAACAGCAGTGAATAAGTA----CTTA 5183
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Db      1421 GAAATCCATTCCATTTTGTGAATTGTGACAAATAACAGCAGTGGAAAAAGTATGTGCTTA 1480

Qy      5184 GAAATGTGAAA-AATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGAT 5242
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      1481 GAATTGTGAAAGAATTAGCAGTAAATACATGAGATAAAGACCTCAAGAAGTTAAAGAT 1540

Qy      5243 AGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATATGCATAC 5302
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Db      1541 ACTTAATTCTTGCCCTTATACCTCACTCTATTCTGTAAATTTGAAAAAAGCATGGATAC 1600

Qy      5303 CTGGATTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAA 5354
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Db      1601 CTGGATATCCTTGGCTTCTTTGAGAATTTAAGAGAAATTAATCTGAATAAA 1652

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## RESULT 2

HSM806642

LOCUS HSM806642 2151 bp mRNA linear HTC 20-JAN-2005

DEFINITION Homo sapiens mRNA; cDNA DKFZp686A13192 (from clone DKFZp686A13192).

ACCESSION BX640600

VERSION BX640600.1 GI:34364600

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 2151)

AUTHORS Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,  
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and  
Wiemann,S.

CONSRM The German cDNA Consortium

TITLE Direct Submission

JOURNAL Submitted (20-JAN-2005) MIPS, Ingolstaedter Landstr.1, D-85764  
Neuherberg, GERMANY

COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by DKFZ (German Cancer Research Center,  
Heidelberg/Germany) within the cDNA sequencing consortium of the  
German Genome Project. This clone (DKFZp686A13192) is available at  
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in  
Berlin, Germany. Please contact RZPD for ordering:  
<http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686A13192>  
Further information about the clone and the sequencing project is  
available at <http://mips.gsf.de/projects/cdna/>.

FEATURES Location/Qualifiers

source 1..2151

/organism="Homo sapiens"

/mol\_type="mRNA"

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/clone="DKFZp686A13192"
/tissue_type="esophagus tumor"
/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
DH10B; sites SfiIA + SfiIB"
/dev_stage="adult"
/note="melanoma antigen, family A, 6"
gene      1. .2151
          /gene="DKFZp686A13192"
CDS       569. .1513
          /gene="DKFZp686A13192"
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          /product="hypothetical protein"
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          /db_xref="GI:34364601"
          /db_xref="InterPro:IPR002190"
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VFGIELMEVDPIGHVYIFATCLGLSYDGLLDNQIMPKTGFLIIILAIKAGDCAPE
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#### ORIGIN

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Query Match      18.3%;  Score 1036.4;  DB 6;  Length 2151;
Best Local Similarity 82.1%;  Pred. No. 1.8e-247;
Matches 1300;  Conservative 0;  Mismatches 251;  Indels 33;  Gaps 8;

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Qy      3816 GCCTGTGGGTCTTCATTGCCAGCTCCTGCCACACTCCTGCCTGCTGCCCTGACCAGAG 3875
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Db      504 GCCAGTGGGTCTCCATTGCCAGCTCCTGCCACACTCCCGCCTGTTGCCCTGACCAGAG 563

Qy      3876 TCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCC 3935
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      564 TCATCATGCCTCTTGAGCAGAGGAGTCAGCACTGCAAGCCTGAAGAAGGCCCTTGAGGCCC 623

Qy      3936 AACAGAGGCCCTGGGCCCTGGTGTGTGTGCAAGCT-----GCCA 3974
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      624 GAGGAGAGGCCCTGGGCCCTGGTGGGTGCGCAGGCTCCTGCTACTGAGGAGCAGGAGGCTG 683

Qy      3975 CCTCCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAA 4034
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      684 CCTCCTCCTCTCTACTCTAGTTGAAGTCACCCTGGGGGAGGTGCCTGCTGCCGAGTCAC 743

Qy      4035 CAGATCCTCCCCAGAGTCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTC 4094
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Db      744 CAGATCCTCCCCAGAGTCTCAGGGAGCCTCCAGCCTCCCCACTACCATGAACCTACCTC 803

Qy      4095 GACAGAGGCAACCCAGTGAGGGTTCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTT 4154
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Qy      4155 GTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTT 4214
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Qy      4215 TTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTG 4274
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Qy	4455	CAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGG	4514
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Qy	4515	AGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCT	4574
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Db	1284	TCGGGGATCCCAAGAAGCTGCTCACCCAATATTTTCGTGCAGGAAAAGTACCTGGAGTACC	1343
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Qy	4694	CTGAAACCAGCTATGTGAAAGTCCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCT	4753
Db	1404	TTGAAACCAGCTATGTGAAAGTCCCTGCACCATATGGTAAAGATCAGTGGAGGACCTCGCA	1463
Qy	4754	TTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCAT	4813
Db	1464	TTTCTTACCACTCCTGCATGAGTGGGCTTTGAGAGAGGGGGAAGAGTGAAGTCTGAGCAC	1523
Qy	4814	GAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCCGCTC	4873
Db	1524	GAGTTGCAGCCAAGGCCAGTGGGAGGGGGTTTGGGCCAGTGCACCTTCCGGGGCCCATC	1583
Qy	4874	CAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCAC TC--TGAAGAGAGCGG	4931
Db	1584	CCTTAGTTTCCACTGCCTCCTGTGACGTGAGGCCCATTCCTTCAC TCTTTGAAGCGAGCAG	1643
Qy	4932	TCAGTGTTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTC	4991
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Qy	4992	TCTTTTGAATTTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCA	5051
Db	1704	CCTGTTGGAGTTGTTCAAATG-TTCCTTTTAACGGATGGTTGAATGAGCGTCAGCATCCA	1762
Qy	5052	AGTTTATGAATGACAGCAGTCACAC--AGTTCTGTGTATATAGTTTAAGGGTAAGAGTCT	5109
Db	1763	GGTTTATGAATGACAGTAGTCACACATAGTGCTGTTTATATAGTTTAGGAGTAAGAGTCT	1822
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Db	1823	TGTTTTTTTATTCAGATTGGGAAATCCATTCCATTTTGTGAATTGTGACATAATAATAGCA	1882
Qy	5168	GTGGAATAAGTACTT-AGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACT	5226

Db	1883	GTGGAAAAAGTATTTGCTTAAATTGTGAGCGAATTAGCAATAACATACATGAGATAACT	1942
Qy	5227	AAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTT 	5286
Db	1943	CAAGAAATCAAAGATAGTTGATTCTTGCCCTGTACCTCAATCTATTCTGTAAAA---TT	1999
Qy	5287	AAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATC 	5346
Db	2000	AAACAAATATGCCAAC CAGGATTTCCTTGACTTCTTTGAGAATGCAAGCGAAATTAAATC	2059
Qy	5347	TGAATAAAGAATTCTTCCTGTTCA	5370
Db	2060	TGAATAAATAATTCTTCCTCTTCA	2083



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Qy	3876	TCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCC	3935
Db	179	TCATCATGTCTTCTGAGCAGAAGAGTCAGCACTGCAAGCCTGAGGAAGGCGTTGAGGCCC	238
Qy	3936	AACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC-----	3975
Db	239	AAGAAGAGGCCCTGGGCCTGGTGGGTGCACAGGCTCCTACTACTGAGGAGCAGGAGGCTG	298
Qy	3976	----CTCCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGT	4031
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Db	359	CAGCAGGTCTCCCCAGAGTCCTCAGGGAGCCTCTGCCTTACCCACTACCATCAGCTTCA	418
Qy	4092	CTCGACAGAGGCAACCCAGTGAGGGTTCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCT	4151
Db	419	CTTGCTGGAGGCAACCCAATGAGGGTTCAGCAGCCAAGAAGAGGAGGGGCCAAGCACCT	478
Qy	4152	CTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTG	4211
Db	479	CGCCTGACGCAGAGTCCTTGTTCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGCTC	538
Qy	4212	GTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGA	4271
Db	539	ATTTTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGA	598
Qy	4272	GTGTCATCAAAAATTACAAGCACTGTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCT	4331
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Db	659	TGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCGCCAGCAACACCTACACCC	718
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Qy	4452	AGACAGGCTTCTGATAATTGTCTTGGTCATGATTGCAATGGAGGGCGCCATGCTCCTG	4511
Db	779	AGACAGGCTTCTGATAATCGTCCTGGGCACAATTGCAATGGAGGGCGACAGCGCCTCTG	838
Qy	4512	AGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTG	4571
Db	839	AGGAGGAAATCTGGGAGGAGCTGGGTGTGATGGGGGTGTATGATGGGAGGGAGCACACTG	898
Qy	4572	CCTATGGGGAGCCCAGGAAGCTGCTCACCAAGATTGGGTGCAGGAAAAGTACCTGGAGT	4631
Db	899	TCTATGGGGAGCCCAGGAAACTGCTCACCAAGATTGGGTGCAGGAAAAGTACCTGGAGT	958
Qy	4632	A-CGGCAGGTGCCGGACAGTGATCCCGCACGTATGAGTTCTGTGGGGTCCAAGGGCCC	4690
Db	959	ACCGGCAGGTACCGGCAGTAATCCTGCGCGCTATGAGTTCTGTGGGGTCCAAGGGCTC	1018
Qy	4691	TCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGAAGAGTTC	4750

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Db      1019 TGGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGGTCAGGGTCAATGCAAGAGTTC 1078
Qy      4751 GCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAG 4810
      || || || |||||
Db      1079 GCATTGCCCTACCCATCCCTGCGTGAAGCAGCTTTGTTAGAGGAGGAAGAGGGAGTCTGAG 1138
Qy      4811 CATGAGTTGCAGCCAAGGCCAGTGGGAGGG----GGACTGGGCCAGTGCACCTTCCAGGG 4866
      ||||| ||| ||| || ||||| || |||
Db      1139 CATGAGTTGCAGCCAGGGCTGTGGGGAAGGGGCAGGGCTGGGCCAGTGCATCTAACA--G 1196
Qy      4867 CCGCGTCCAGCAGCTTCCCTGCGTCGTGTGACATGAGGCCCATCTTCACTC----TGA 4922
      || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1197 CCCTGTGCAGCAGCTTCCCTTGCCTCGTGTAAACATGAGGCCCATCTTCACTCTGTTTGA 1256
Qy      4923 AGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTA 4982
      ||| | ||||| ||||| ||||| || ||||| ||||| |||||
Db      1257 AGAAAATAGTCAGTGTTCTTAGTAGTGGGTTTCTATTTTGTGGATGACTTGGAGATTTA 1316
Qy      4983 TCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTT 5042
      ||| |||| |||| ||||| ||||| || ||||| ||||| |||||
Db      1317 TCCTGTGTTCCCTTTTACAATTGTTGAAATG--TTCCTTTAATGGATGGTTGAATTAACCTT 1375
Qy      5043 CAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTA 5102
      ||||| ||||| ||||| || || || || ||||| ||||| |||||
Db      1376 CAGCATCCAAGTTTATGAATCGTAGTTAACGTATATTGCTGTTAATATAGTTTAGGAGTA 1435
Qy      5103 AGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCATTTTGTGAATTGGG---ATAA 5159
      ||||| ||||| ||||| ||||| ||||| ||||| || |||||
Db      1436 AGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCGTTCTATTTTGTGAATTGGGACATAA 1495
Qy      5160 TAACAGCAGTGGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATA 5219
      ||||| ||||| ||||| |||| |||| || || ||||| |||||
Db      1496 TAACAGCAGTGGAGTAAGTATTTAGAAGTGTG---AATTCACCGTGAAATAGGTGAGAT- 1551
Qy      5220 AAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAA 5279
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1552 -----AAATTAAGATACTTAATTCCCGCCTTATGCCTCAGTCTATTCTGTAA 1600
Qy      5280 AATTT-TTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAA 5338
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1601 AATTTAAAAAATATATATGCATACCTGGATTTCCTTGGCTTC---GTGAATGTAAGAGAA 1657
Qy      5339 ATTAAATCTGAATA 5352
      ||||| |||||
Db      1658 ATTAAATCTGAATA 1671

```

#### RESULT 4

CR595748

LOCUS CR595748 1689 bp mRNA linear HTC 21-JUL-2004

DEFINITION full-length cDNA clone CS0DK007YN24 of HeLa cells Cot 25-normalized of Homo sapiens (human).

ACCESSION CR595748

VERSION CR595748.1 GI:50476555

KEYWORDS HTC; CNSLT\_cDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1689)

<http://es/ScoreAccessWeb/GetItem.action?AppId=08819669&seqId=610474&ItemName=us...> 8/30/06

Db 536 TTCTGCTCCTCAAGTATCGAGCCAGGGAGCCGGTCACAAAGGCAGAAATGCTGGGGAGTG 595

Qy 4275 TCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGC 4334  
 || || ||||| || ||| ||||| ||||| ||||| || || |||||

Db 596 TCGTCGGAAATTGGCAGTACTTCTTTCTGTGATCTTCAGCAAAGCTTCCGATTCTTGC 655

Qy 4335 AGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTG 4394  
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Db 656 AGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTG 715

Qy 4395 TCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGA 4454  
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Db 716 CCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAAGA 775

Qy 4455 CAGGCTTCCTGATAAATGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGG 4514  
 ||||| ||||| ||||| ||||| ||||| ||||| || || |||||

Db 776 CAGGCTTCCTGATAATCATCCTGGCCATAATCGCAAAAGAGGGCGACTGTGCCCTGAGG 835

Qy 4515 AGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCT 4574  
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

Db 836 AGAAAATCTGGGAGGAGCTGAGTGTGTTAGAGGTGTTTGAGGGGAGGGAAGACAGTATCT 895

Qy 4575 ATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-C 4633  
 |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||

Db 896 TCGGGGATCCCAAGAAGCTGCTCACCCAATATTTCTGTCAGGAAAACCTACCTGGAGTACC 955

Qy 4634 GGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCG 4693  
 ||||| || || ||||| ||||| ||||| ||||| ||||| |||||

Db 956 GGCAGGTCCCCGGCAGTGATCCTGCATGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCA 1015

Qy 4694 CTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTTCGCT 4753  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1016 TTGAAACCAGCTATGTGAAAGTCCTGCACCATATGGTAAAGATCAGTGGAGGACCTCGCA 1075

Qy 4754 TTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCAT 4813  
 |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||

Db 1076 TTTCTTACCCACTCCTGCATGAGTGGGCTTTGAGAGAGGGGAAGAGTGAGTCTGAGCAC 1135

Qy 4814 GAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTC 4873  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

Db 1136 GAGTTGCAGCCAGGGCAGTGGGAGGGGGTTTGGGCCAGTGCACCTTCCGGGGCCCCATC 1195

Qy 4874 CAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTC--TGAAGAGAGCGG 4931  
 | || |||| ||||| ||||| ||||| ||||| ||||| ||||| ||

Db 1196 CCTTAGTTTCCACTGCCTCCTGTGACGTGAGGCCATTCTTCACTCTTTGAAGCGAGCAG 1255

Qy 4932 TCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTT 4991  
 |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||

Db 1256 TCAGCATTTCTTAGTAGTGGGTTTCTGTTCTGTTGGATGACTTTGAGATTATCTTTGTTT 1315

Qy 4992 TCTTTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCA 5051  
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1316 CCTGTTGGAGTTGTTCAAATG-TTCCTTTTAACGGATGGTTGAATGAGCGTCAGCATCCA 1374

Qy 5052 AGTTTATGAATGACAGCAGTCACAC--AGTTCTGTGTATATAGTTTAAGGGTAAGAGTCT 5109  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1375 GGTTTATGAATGACAGTAGTCACACATAGTGTGTTTATATAGTTTAGGAGTAAGAGTCT 1434

Qy 5110 TGTGTTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGG--ATAATAACAGCA 5167  
 ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1435 TGTTTTTTTATTTCAGATTGGGAAATCCATTCCATTTTGTGAATTGTGACATAATAATAGCA 1494

Qy	5168	GTGGAATAAGTACTT-AGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACT	5226
Db	1495	GTGGAAAAAGTATTTGCTTAAATTTGTGAGCGAATTAGCAATAACATACATGAGATAACT	1554
Qy	5227	AAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTT	5286
Db	1555	CAAGAAATCAAAGATAGTTGATTCTTGCCCTGTACCTCAATCTATTCTGTAAAA---TT	1611
Qy	5287	AAAGATATATGCATACCTGGATTTCTTGCGCTCTTTGAGAATGTAAGAGAAATTAAATC	5346
Db	1612	AAACAAATATGCAACCAGGATTTCTTGACTTCTTTGAGAATGCAAGCGAAATTAAATC	1671
Qy	5347	TGAATAAAGAATTCTTCC	5364
Db	1672	TGAATAAATAATTCTTCC	1689

Matches 1308; Conservative 0; Mismatches 196; Indels 58; Gaps 11;

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Qy      3816 GCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCTGCCTGCTGCCCTGACGAGAG 3875
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Db      198 GCCTGTGGGTCCCCATTGCCCAGCTTTTGCCTGCACTCTTGCCCTGCTGCCCTGACCAGAG 257

Qy      3876 TCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCC 3935
          |||||
Db      258 TCATCATGTCTCTTGAGCAGAAGAGTCAGCACTGCAAGCCTGAGGAAGGCGTTGAGGCCC 317

Qy      3936 AACAAAGAGGCCCTGGGCTGGTGTGTGTGCAGGCTGCCAC----- 3975
          |||||
Db      318 AAGAAGAGGCCCTGGGCTGGTGGGTGCACAGGCTCCTACTACTGAGGAGCAGGAGGCTG 377

Qy      3976 ----CTCCTCCTCCTCCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGT 4031
          |||||
Db      378 CTGTCTCCTCCTCCTCCTCCTCTGGTCCCTGGCACCTGGAGGAAGTGCTGCTGCTGAGT 437

Qy      4032 CAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCA 4091
          |||||
Db      438 CAGCAGGTCTCCTCCCCAGAGTCCTCAGGGAGCCTCTGCCTTACCACTACCATCAGCTTCA 497

Qy      4092 CTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGGCCAAGCACCT 4151
          |||||
Db      498 CTTGCTGGAGGCAACCCAATGAGGGTTCCAGCAGCCAAGAAGAGGAGGGGGCCAAGCACCT 557

Qy      4152 CTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTG 4211
          |||||
Db      558 CGCCTGACGCAGAGTCCTTGTTCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGCTC 617

Qy      4212 GTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGA 4271
          |||||
Db      618 ATTTTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGA 677

Qy      4272 GTGTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCT 4331
          |||||
Db      678 GAGTCATCAAAAATTACAAGCGCTGCTTTCTGTGATCTTCGGCAAAGCCTCCGAGTCCC 737

Qy      4332 TGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCC 4391
          |||||
Db      738 TGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCGCCAGCAACACCTACACCC 797

Qy      4392 TTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCA 4451
          |||||
Db      798 TTGTCACCTGCCTGGGCCCTTCCTATGATGGCCTGCTGGGTAATAATCAGATCTTTCCCA 857

Qy      4452 AGACAGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTG 4511
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Db      858 AGACAGGCCTTCCTGATAATCGTCTGGGCACAATTGCAATGGAGGGCGACAGCGCCTCTG 917

Qy      4512 AGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTG 4571
          |||||
Db      918 AGGAGGAAATCTGGGAGGAGCTGGGTGTGATGGGGGTGTATGATGGGAGGGAGCACACTG 977

Qy      4572 CCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAAGTACCTGGAGT 4631
          |||||
Db      978 TCTATGGGGAGCCCAGGAACTGCTCACCCAAGATTGGGTGCAGGAAAAGTACCTGGAGT 1037

Qy      4632 A-CGGCAGGTGCCGGACAGTGATCCCGCAGCTATGAGTTCCTGTGGGGTCCAAGGGCCC 4690
          |||||
Db      1038 ACCGGCAGGTACCGGCAGTAATCCTGCGCGCTATGAGTTCCTGTGGGGTCCAAGGGCTC 1097
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Qy	4691	TCGCTGAAACACAGCTATGTGAAAAGTCCTTGAGATGTGATCAAGGTCAGTGC AAGAGTTC	4750
Db	1098	TGGCTGAAACACAGCTATGTGAAAAGTCCTTGAGCATGTGGTCAGGGTCAATGCAAGAGTTC	1157
Qy	4751	GCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAG	4810
Db	1158	GCATTGCCTACCCATCCCTGCGTGAAGCAGCTTTGTTAGAGGAGGAAGAGGGAGTCTGAG	1217
Qy	4811	CATGAGTTGCAGCCAAGGCCAGTGGGAGGG---GGACTGGGCCAGTGCACCTTCCAGGG	4866
Db	1218	CATGAGTTGCAGCCAGGGCTGTGGGGAAGGGGCAGGGCTGGGCCAGTGCATCTAACA--G	1275
Qy	4867	CCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTC---TGA	4922
Db	1276	CCCTGTGCAGCAGCTTCCCCTGCCTCGTGTAAACATGAGGCCCATCTTCACTCTGTTTGA	1335
Qy	4923	AGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCCTATTGGGTGACTTGGAGATTTA	4982
Db	1336	AGAAAATAGTCAGTGTCTTAGTAGTGGGTTTCTATTTTGTGGATGACTTGGAGATTTA	1395
Qy	4983	TCTTTGTTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TT	5042
Db	1396	TCTCTGTTTCCTTTTACAATTGTTGAAATG-TTCCTTTTAATGGATGGTTGAATTAAC TT	1454
Qy	5043	CAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAAGGGTA	5102
Db	1455	CAGCATCCAAGTTTATGAATCGTAGTTAACGTATATTGCTGTTAATATAGTTTAGGAGTA	1514
Qy	5103	AGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGG---ATAA	5159
Db	1515	AGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCGTTCTATTTTGTGAATTGGGGACATAA	1574
Qy	5160	TAACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATA	5219
Db	1575	TAACAGCAGTGGAGTAAGTATTTAGAAGTGTG---AATTCACCGTGAAATAGGTGAGAT-	1630
Qy	5220	AAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAA	5279
Db	1631	-----AAATTAAGAGATACTTAATCCCGCCTTATGCCTCAGTCTATTCTGTAA	1679
Qy	5280	AATTT-TTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAA	5338
Db	1680	AATTTAAAAATATATATGCATACCTGGATTTCCTTGGCTTC--GTGAATGTAAGAGAA	1736
Qy	5339	AT 5340	
Db	1737	AT 1738	

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 1661)  
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600  
Faraday Avenue

REFERENCE 2 (bases 1 to 1661)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.

FEATURES Location/Qualifiers  
source 1. .1661  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DC020YG12"  
/tissue\_type="Neuroblastoma Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"

# ORIGIN

Query Match 17.8%; Score 1008.6; DB 6; Length 1661;  
Best Local Similarity 81.8%; Pred. No. 1.6e-240;  
Matches 1271; Conservative 0; Mismatches 249; Indels 33; Gaps 8;

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Qy      3816 GCCTGTGGGTCTTCATTGCCCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAG 3875
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      113 GCCAGTGGGTCTCCATTGCCCCAGCTCCTGCCCACACTCCCGCCTGTTGCCCTGACGAGAG 172

Qy      3876 TCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCC 3935
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      173 TCATCATGCCCTTGAGCAGAGGAGTCAGCACTGCAAGCCTGAAGAAGCCCTTGAGGCCC 232

Qy      3936 AACAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCT-----GCCA 3974
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      233 GAGGAGAGGCCCTGGGCCTGGTGGGTGCGCAGGCTCTGCTACTGAGGAGCAGGAGGCTG 292

Qy      3975 CCTCCTCCTCCTCCTCCTCCTGCTGCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAA 4034
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      293 CCTCCTCCTCCTCCTCCTCCTGCTGCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAA 352

Qy      4035 CAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTC 4094
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      353 CAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCAGCCTCCCCACTACCATGAAGTACCTC 412

Qy      4095 GACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTT 4154
          ||| ||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      413 TCTGGAGCCAATCTATGAGGACTCCAGCAACCAAGAAGAGGAGGGGCCAAGCACCTTCC 472

Qy      4155 GTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTT 4214
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      473 CTGACCTGGAGTCTGAGTTCCAAGCAGCACTCAGTAGGAAGGTGGCCAAGTTGGTTTCATT 532

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Qy	4215	TTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTG	4274
Db	533	TTCTGCTCCTCAAGTATCGAGCCAGGGAGCCGGTCACAAAGGCAGAAATGCTGGGGAGTG	592
Qy	4275	TCATCAAAAATTACAAGCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGC	4334
Db	593	TCGTCGGAAATTGGCAGTACTTCTTTCCTGTGATCTTCAGCAAAGCTCCGATTCTTGC	652
Qy	4335	AGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGCCACTCCTATGTCCTTG	4394
Db	653	AGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCATCGGCCACGTGTACATCTTG	712
Qy	4395	TCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCAAGA	4454
Db	713	CCACCTGCCTGGGCCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCAAGA	772
Qy	4455	CAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGG	4514
Db	773	CAGGCTTCCTGATAATCATCCTGGCCATAATCGCAAAAGAGGGCGACTGTGCCCTGAGG	832
Qy	4515	AGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCT	4574
Db	833	AGAAAATCTGGGAGGAGCTGAGTGTGTTAGAGGTGTTTGAGGGGAGGGAAGACAGTATCT	892
Qy	4575	ATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-C	4633
Db	893	TCGGGGATCCCAAGAAGCTGCTCACCCAATATTTCTGTCAGGAAAAGTACCTGGAGTACC	952
Qy	4634	GGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCG	4693
Db	953	GGCAGGTCCCCGGCAGTGATCCTGCATGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCA	1012
Qy	4694	CTGAAACCAGCTATGTGAAAGTCCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTTCGCT	4753
Db	1013	TTGAAACCAGCTATGTGAAAGTCCGTCACCATATGGTAAAGATCAGTGGAGGACCTCGCA	1072
Qy	4754	TTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCAT	4813
Db	1073	TTTCTTACCACTCCTGCATGAGTGGGCTTTGAGAGAGGGGGAAGAGTGAGTCTGAGCAC	1132
Qy	4814	GAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTC	4873
Db	1133	GAGTTGCAGCCAGGGCCAGTGGGAGGGGGTTTGGGCCAGTGCACCTTCCGGGGCCCCATC	1192
Qy	4874	CAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTTCAC TC--TGAAGAGAGCGG	4931
Db	1193	CCTTAGTTTCCACTGCCTCCTGTGACGTGAGGCCATTCTTCAC TCTTTGAAGCGAGCAG	1252
Qy	4932	TCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTC	4991
Db	1253	TCAGCATTCTTAGTAGTGGGTTTCTGTTCTGTTGGATGACTTTGAGATTATCTTTGTTT	1312
Qy	4992	TCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCA	5051
Db	1313	CCTGTTGGAGTTGTTCAAATG-TTCCTTTTAACGGATGGTTGAATGAGCGTCAGCATCCA	1371
Qy	5052	AGTTTATGAATGACAGCAGTCACAC--AGTTCTGTGTATATAGTTTAAGGGTAAGAGTCT	5109
Db	1372	GGTTTATGAATGACAGTAGTCACACATAGTGCTGTTTATATAGTTTAGGAGTAAGAGTCT	1431

Qy	5110	TGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGG--ATAATAACAGCA	5167
Db	1432	TGTTTTTTTATTTCAGATTGGGAAATCCATTCATTTTGTGAATTGTGACATAATAATAGCA	1491
Qy	5168	GTGGAATAAGTACTT-AGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACT	5226
Db	1492	GTGGAATAAGTATTTGCTTAAATTTGTGAGCGAATTAGCAATAACATACATGAGATAACT	1551
Qy	5227	AAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAAAATTTT	5286
Db	1552	CAAGAAATCAAAAGATAGTTGATTCTTGCCCTGTACCTCAATCTATTCTGTAAAA---TT	1608
Qy	5287	AAAGATATATGCATACCTGGATTTCCTTGCCCTCTTTGAGAATGTAAGAGAAA	5339
Db	1609	AAACAAATATGCCAACAGGATTTCCTTGACTTCTTTGAGAATGCAAGCGAAA	1661

Matches 929; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	3881	ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA	3940
Db	1	ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA	60
Qy	3941	GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCCTG	4000
Db	61	GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCCTG	120
Qy	4001	GGCACCTTGAGGAGGTGCCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA	4060
Db	121	GGCACCTTGAGGAGGTGCCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA	180
Qy	4061	GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC	4120
Db	181	GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC	240
Qy	4121	AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCA	4180
Db	241	AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCA	300
Qy	4181	GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG	4240
Db	301	GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG	360
Qy	4241	GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTT	4300
Db	361	GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTT	420
Qy	4301	CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCACTGCTTGGCATTGACGTGAAG	4360
Db	421	CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCACTGCTTGGCATTGACGTGAAG	480
Qy	4361	GAAGCAGACCCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGAT	4420
Db	481	GAAGCAGACCCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGAT	540
Qy	4421	GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC	4480
Db	541	GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC	600
Qy	4481	ATGATTGCAATGGAGGGCGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG	4540
Db	601	ATGATTGCAATGGAGGGCGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG	660
Qy	4541	ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACC	4600
Db	661	ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACC	720
Qy	4601	CAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCA	4659
Db	721	CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA	780
Qy	4660	CGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT	4719
Db	781	CGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT	840
Qy	4720	GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA	4779
Db	841	GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA	900

Qy 4780 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGA 4809  
 |||  
 Db 901 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGA 930

# RESULT 8

BM459064

LOCUS BM459064 1020 bp mRNA linear EST 05-FEB-2002

DEFINITION AGENCOURT\_6414460 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:5557380  
 5', mRNA sequence.

ACCESSION BM459064

VERSION BM459064.1 GI:18508104

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 1020)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: ATCC/DCTD/DTP

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM12278 row: k column: 13

High quality sequence stop: 605.

## FEATURES

source

Location/Qualifiers

1..1020

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5557380"

/tissue\_type="melanotic melanoma"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_72"

/note="Organ: skin; Vector: pCMV-SPORT6; Site\_1: NotI;

Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2 kb. Library constructed by Life  
 Technologies."

## ORIGIN

Query Match 14.8%; Score 840.2; DB 2; Length 1020;

Best Local Similarity 97.8%; Pred. No. 2.1e-198;

Matches 870; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

Qy 4411 CTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT 4470  
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Db 1 CTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT 60

Qy 4471 TGTCTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGA 4530  
 |||

Db 61 TGTCTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGA 120

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Qy      4531 GCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAA 4590
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Db      121 GCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAA 180

Qy      4591 GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAG 4649
          |||
Db      181 GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAG 240

Qy      4650 TGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGT 4709
          |||
Db      241 TGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTTGCTGAAACCAGCTATGT 300

Qy      4710 GAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCT 4769
          |||
Db      301 GAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCT 360

Qy      4770 GCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGC 4829
          |||
Db      361 GCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGC 420

Qy      4830 CAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGC 4889
          |||
Db      421 CAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGC 480

Qy      4890 CTCGTGTGACATGAGGCCCATTCCTTCACTCTGAAGAGAGCGGTCAGTGTCTCAGTAGTA 4949
          |||
Db      481 CTCGTGTGACATGAGGCCCATTCCTTCACTCTGAAGAGAGCGGTCAGTGTCTCAGTAGTA 540

Qy      4950 GGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGGAATTGTTCAA 5009
          |||
Db      541 GGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGGAATTGTTCAA 600

Qy      5010 ATGTTTTTTTTTAAAGGGATGGTTGAATGAACCTCAGCATCCAAGTTTATGAATGACAGCA 5069
          |||
Db      601 ATGTTTTTTTTTAAAGGGATGGTTGAATGAACCTCAGCATCCAAGTTTATGAATGACAGCA 660

Qy      5070 GTCACACAGTTCTGTGTATATAGTTTAAAGGTAAGAGTCTTGTGTTTTATTTCAGATTGGG 5129
          |||
Db      661 GTCGCACAGTTCTGTGTATATAGTTTAAAGGTAAGAGTCTTGTGTTTTATTTCAGATTGNG 720

Qy      5130 AAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGAATAAGTACTTAGAAAATG 5189
          |||
Db      721 AAATCCATTCTATTTTGTGAATTGGGAACATAACAGCAGTGAATAAGTACTTAGAATG 780

Qy      5190 TGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAAT 5249
          |
Db      781 TNGAAAATGAGCANGTAAATAGATGAGATAAAGAACTANAGAAATTAAGAGATAGTCAAT 840

Qy      5250 TCTTGCC-TTATACCTCAGTCTATTCTGTAAAATTTTTAAAGATATATGC 5298
          |||
Db      841 TCTTGCCTTTATACCTCCGCCTATTCTGTAAAATTTTTAAAGATATATGC 890

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RESULT 9  
DQ034886

LOCUS DQ034886 923 bp DNA linear GSS 02-JUN-2005  
DEFINITION Pan troglodytes MAGEA1 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION DQ034886  
VERSION DQ034886.1 GI:66886095  
KEYWORDS GSS.

[illegible]

Qy 4244 CCAGTCACAAAGGCAGAAATGCTGGAGAGTGTTCATCAAAAAATTACAAGCACTGTTTTCTCT 4303  
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 Db 361 CCAGTCACAAAGGCAGAAATGCTGGAGAGTGTTCATCAAAAAATTACAAGCACTGTTTTCTCT 420  
 Qy 4304 GAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAA 4363  
 | |||  
 Db 421 GTGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGAGGTGAAGGAA 480  
 Qy 4364 GCAGACCCCAACGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGC 4423  
 |||  
 Db 481 GCAGACCCCAACGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTACGATGGC 540  
 Qy 4424 CTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATG 4483  
 |||  
 Db 541 CTGCTGGGAGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATG 600  
 Qy 4484 ATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATG 4543  
 |||  
 Db 601 ATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATG 660  
 Qy 4544 GAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAA 4603  
 |||  
 Db 661 GAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAA 720  
 Qy 4604 GATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGC 4662  
 |||  
 Db 721 GATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCACGC 780  
 Qy 4663 TATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAG 4722  
 |||  
 Db 781 TATGAGTNNCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAANNCTTGAG 840  
 Qy 4723 TATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCT 4782  
 |||  
 Db 841 TATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGANGNAGCT 900  
 Qy 4783 TTGAGAGAGGAGGAAGAGGGAGT 4805  
 |||  
 Db 901 TTGAGAGAGGAGGAAGAGGGAGT 923

# RESULT 10

CR619399

LOCUS CR619399 1739 bp mRNA linear HTC 21-JUL-2004

DEFINITION full-length cDNA clone CS0DI079YD09 of Placenta Cot 25-normalized of Homo sapiens (human).

ACCESSION CR619399

VERSION CR619399.1 GI:50500206

KEYWORDS HTC; CNSLT\_cDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1739)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ InVitroGen Corporation 1600  
 Faraday Avenue

REFERENCE 2 (bases 1 to 1739)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
FEATURES Location/Qualifiers  
source 1. .1739  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DI079YD09"  
/tissue\_type="Placenta Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"

# ORIGIN

Query Match 13.8%; Score 783.6; DB 6; Length 1739;  
Best Local Similarity 77.1%; Pred. No. 3.6e-184;  
Matches 1190; Conservative 0; Mismatches 244; Indels 110; Gaps 15;

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Qy      3816 GCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAG 3875
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Db      151 GCCTGTGGGTCTCAATTGCCCAGCTCCGGCCCACACTCT--CCTGCTGCCCTGACCTGAG 208

Qy      3876 TCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCC 3935
          |||||
Db      209 TCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCC 268

Qy      3936 AACAGAGGCCCTGGGCTGGTGTGTGTGCAGGCTGCCA----- 3974
          || |||||
Db      269 AAGGAGAGGCACCAGGGCTTATGGATGTGCAGATTCCCACAGCTGAGGAGCAGAAGGCTG 328

Qy      3975 CCTCCTCCTCCTCCTCCTCCTGCTGCTGGGACCCCTGGAGGAGGTGCCCACTGCTGGGTCAA 4034
          | |||||
Db      329 CATCCTCCTCCTCCTCCTCCTGCTGCTGGGACCCCTGGAGGAGGTGCCCACTGCTGGGTCAA 388

Qy      4035 CAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTC 4094
          || |||||
Db      389 CAAGTCCTCCCCAGAGTCCTCAGGGGTGCCTCCTCCTCCCTGACTGTCACCGACAGCACTC 448

Qy      4095 GACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCT--- 4151
          ||| ||| || |||||
Db      449 TGTGGAGCCAATCCGATGAGGGTTCCAGCAGCAATGAAGAGGAGGGGCCAAGCACCTCCC 508

Qy      4152 -----CTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATT 4205
          | | |||||
Db      509 CGGACCCAGCTCACCTGGAGTCCCTGTTCCGGAAGCACTTGATGAGAAAGTGGCTGAGT 568

Qy      4206 TGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGC 4265
          | ||| ||| |||||
Db      569 TAGTTTCGTTTCTGCTCCGCAAATATCAAATTAAGGAGCCGGTCACAAAGGCAGAAATGC 628

Qy      4266 TGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTTCTGAGATCTTCGGCAAAGCCTCTG 4325
          | |||||
Db      629 TTGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTTCTGAGATCTTCGGCAAAGCCTCTG 688

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Qy	4326	AGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCT	4385
Db	689	AGTGCATGCAGGTGATCTTTGGCATTGATGTGAAGGAAGTGGACCTGCCGGCCACTCCT	748
Qy	4386	ATGTCCTTGTACCTGCCTAGGTCCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCA	4445
Db	749	ACATCCTTGTACCTGCCTGGGCCTCTCCTATGATGGCCTGCTGGGTGATGATCAGAGTA	808
Qy	4446	TGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATG	4505
Db	809	CGCCCAAGACCGGCTTCCTGATAATCGTCCTGGGCATGATCTTAATGGAGGGCAGCCGCG	868
Qy	4506	CTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGC	4565
Db	869	CCCCGGAGGAGGCAATCTGGGAAGCATTGAGTGTGATGGGGCTGTATGATGGGAGGGAGC	928
Qy	4566	ACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACC	4625
Db	929	ACAGTGTCTATTGGAAGCTCAGGAAGCTGCTCACCCAAGAGTGGGTGCAGGAGAAGTACC	988
Qy	4626	TGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAA	4684
Db	989	TGGAGTACCGCCAGGCGCCGGCAGTGATCCTGTGCGCTACGAGTTCCTGTGGGGTCCAA	1048
Qy	4685	GGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAA	4744
Db	1049	GGGCCCTTGTCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGGTCAGGGTCAATGCAA	1108
Qy	4745	GAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAG	4804
Db	1109	GAGTTCGATTTTCTTACCCATCCCTGCATGAAGAGGCTTTGGGAGAGGAGAAA--GGAG	1165
Qy	4805	TCTGAGCATGAGTTGCAGCCAAGGCCAGTGG-----GAGGGGACTTGGGCCAGTG	4854
Db	1166	TTTGAGCAGGAGTTGCAGCTAGGGCCAGTGGGGCAGGTTGTGGGAGGGCCTTGGGCCAGTG	1225
Qy	4855	CACCTTCCAGGGCCGCGTCCAGCAGCTTCCCTTGCTCGTGTGACATGAGGCCCATTCCTT	4914
Db	1226	CACGTTCCAGGGCCACATCCACCACTTTCCCTGCTC--TGTTACATGAGGCCCATTCCTT	1282
Qy	4915	CACCTC-----TGAAGAGAGCGGTGAGTGTCTCAGTAGTAG-----	4950
Db	1283	CACCTCTGTGTTTGAAGAGAGCAGTCACAGTTCCTCAGTAGTGGGAGCATGTTGGGTGTGA	1342
Qy	4951	-----GTTTCTGTCTATTGGGTGACTTGGAGATTTATC	4984
Db	1343	GGGAACACAGTGTGGACCATCTCTCAGTTCCTGTCTATTGGGCGATTTGGAGGTTTATC	1402
Qy	4985	TTTGTTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAGTTCA	5044
Db	1403	TTTGTTCTCTTTTGGAAATTGTTCAAATG-TTCCTTCTAATGGATGGTGTAAATGAAGTTCA	1461
Qy	5045	GCATCCAAGTTTATGAATGACAGCAGTCACAC--AGTTCCTGTGTATATAGTTTAAAGGGTA	5102
Db	1462	ACATTC-ATTTTATGTATGACAGTAGACAGACTTACTGCTTTTTATATAGTTTAAAGGGTA	1520
Qy	5103	AGAGTCTTGTGTTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATA--AT	5160
Db	1521	AGAGTCTTGTGTTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATA--AT	1580
Qy	5161	AACAGCAGTGGAAATAAG---TACTTAGAAATGTGAA--AAATGAGCAGTAAAATAGATGA	5215

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      || ||||| ||| |||| | ||||| ||||| ||| ||||| ||||| ||||
Db      1581 AAGAGCAGAGGATTAAGGTTTTTTTAGAAATGTGAAACAACATAGCAGTAAAATACATGA 1640

Qy      5216 GATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTA 5259
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1641 GATAAAGACATAAAGAAATTAACAATAGTTAATTCTTGCCTTA 1684

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# RESULT 11

BU157186

LOCUS BU157186 909 bp mRNA linear EST 04-SEP-2002

DEFINITION AGENCOURT\_7941457 NIH\_MGC\_68 Homo sapiens cDNA clone IMAGE:6011608  
5', mRNA sequence.

ACCESSION BU157186

VERSION BU157186.1 GI:22670718

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 909)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: DCTD/DTP/Gazdar

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM13201 row: i column: 17

High quality sequence start: 18

High quality sequence stop: 583.

## FEATURES

source

Location/Qualifiers

1. .909

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6011608"

/tissue\_type="large cell carcinoma"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_68"

/note="Organ: lung; Vector: pCMV-SPORT6; Site\_1: NotI;

Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.8 kb. Library constructed by Life  
Technologies. "

## ORIGIN

Query Match 13.0%; Score 740.2; DB 3; Length 909;

Best Local Similarity 97.0%; Pred. No. 2.2e-173;

Matches 765; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

Qy 3816 GCCTGTGGGTCTTCATTGCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAG 3875

Db 40 GCCTGTGGGTCTTCATTGCCAGCTCCTGCCCACACTCCTGCCTGTTGCCCTGACGAGAG 99

Qy 3876 TCATCATGTCTCTTGAGCAGAGGAGTCTGCAAGCCTGAGGAAGCCCTTGAGGCCC 3935

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Db      100 TCATCATGTCTCTTGAGCAGAGGAGTCTGCAAGCCTGAGGAAGCCCTTGAGGCC 159
Qy      3936 AACAAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCCTCTGG 3995
Db      160 AACAAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCGCCTCCTCCTCCTCCTCTGG 219
Qy      3996 TCCTGGGCACCCCTGGAGGAGGTGCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTC 4055
Db      220 TCCTGGGCACCCCTGGAGGAGGTGCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTC 279
Qy      4056 AGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGG 4115
Db      280 AGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCAACAGAGGCAACCCAGTGAGG 339
Qy      4116 GTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCC 4175
Db      340 GTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCC 399
Qy      4176 GAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTCTGCTCCTCAAATATCGAG 4235
Db      400 GAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTCTGCTCCTCAAATATCGAG 459
Qy      4236 CCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCAATCAAAAATTACAAGCACT 4295
Db      460 CCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCAATCAAAAATTACAAGCACT 519
Qy      4296 GTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACG 4355
Db      520 GTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACG 579
Qy      4356 TGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCT 4415
Db      580 TGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCT 639
Qy      4416 ATGATGGCCTGCTGGGTGATAATCAGATCATGCCAAGACAGGCTTCCTGATAATTGTCC 4475
Db      640 ATGATGGCCTGCTGGGTGATAATCAGATCATGCCAAGACAGGTTTCTGATAATTGGCC 699
Qy      4476 TGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGA 4535
Db      700 TGGTCCTGATTGCAATGGAAGGGGGCCATGCTCCTGGAGAGGAAATCTGGGACGACCTGA 759
Qy      4536 GTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTG-CCTATGGGGAGCCCAGGAAGCTG 4594
Db      760 ATGTGATGGAGGTGTATGATGGGAAGGAGCCCAGGGCCCTATGGGGAGCCCAGAACTG. 819
Qy      4595 CTCACCCAA 4603
Db      820 CTCCACCCA 828

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RESULT 12  
CA428506/c

LOCUS CA428506 747 bp mRNA linear EST 07-NOV-2002  
DEFINITION UI-H-FE1-bez-g-10-0-UI.s1 NCI\_CGAP\_FE1 Homo sapiens cDNA clone  
UI-H-FE1-bez-g-10-0-UI 3', mRNA sequence.  
ACCESSION CA428506  
VERSION CA428506.1 GI:24791232  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 747)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: James Martin  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained  
from Dr. M. Bento Soares, [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES Location/Qualifiers

source 1. .747  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FE1-bez-g-10-0-UI"  
/tissue\_type="Cell lines"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI\_CGAP\_FE1"  
/note="Organ: Chondrosarcoma; Vector: pT7T3-Pac  
(Pharmacia) with a modified polylinker; Site\_1: EcoR I;  
Site\_2: Not I; NCI\_CGAP\_FE1 is a normalized cDNA library  
derived from a pool of mRNA obtained from 3 cell lines  
from grade II chondrosarcoma tissues. The library was  
constructed according to Bonaldo, Lennon and Soares,  
Genome Research, 6:791-806, 1996. First strand cDNA  
synthesis was primed with an oligo-dT primer containing a  
Not I site. Double stranded cDNA was ligated to an EcoR I  
adaptor, digested with Not I, and cloned directionally  
into pT7T3-Pac vector. The oligonucleotide used to prime  
the synthesis of first-strand cDNA contains a library tag  
sequence that is located between the Not I site and the  
(dT)18 tail. The sequence tag for this library is  
CGCTACGGAC. The cell lines were provided by Dr James  
Martin from the University of Iowa.  
TAG\_TISSUE=Human grade 2 chondrosarcoma cell line pool  
TAG\_LIB=UI-H-FE1  
TAG\_SEQ=CGCTACGGAC"

# ORIGIN

Query Match 12.7%; Score 720.2; DB 4; Length 747;  
Best Local Similarity 99.6%; Pred. No. 2.2e-168;  
Matches 722; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      4633 CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTC 4692
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Db       737 CGGCAGTGCCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTC 678

QY      4693 GCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGC 4752
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Db       677 GCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGC 618

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Qy	4753	TTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCA	4812
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Qy	4813	TGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGT	4872
Db	557	TGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGT	498
Qy	4873	CCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGT	4932
Db	497	CCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGT	438
Qy	4933	CAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCT	4992
Db	437	CAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCT	378
Qy	4993	CTTTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAA	5052
Db	377	CTTTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAA	318
Qy	5053	GTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGT	5112
Db	317	GTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGT	258
Qy	5113	GTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGA	5172
Db	257	GTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGA	198
Qy	5173	ATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAA	5232
Db	197	ATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAA	138
Qy	5233	ATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAAATTTTAAAGAT	5292
Db	137	ATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAAATTTTAAAGAT	78
Qy	5293	ATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATA	5352
Db	77	ATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATA	18
Qy	5353	AAGAA	5357
Db	17	AAGAA	13

# RESULT 13

DQ049942

LOCUS DQ049942 954 bp DNA linear GSS 02-JUN-2005

DEFINITION Homo sapiens MAGEA4 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION DQ049942

VERSION DQ049942.1 GI:66903141

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE 1 (bases 1 to 954)

AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,

Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,  
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and  
Chimpanzees  
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)  
PUBMED 15869325  
REFERENCE 2 (bases 1 to 954)  
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,  
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,  
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment. Translation starts at the beginning of  
alignment.

FEATURES Location/Qualifiers  
source 1. .954  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
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/chromosome="X"  
gene <1. .>954  
/gene="MAGEA4"  
/locus\_tag="HC17937"

#### ORIGIN

Query Match 12.3%; Score 700; DB 14; Length 954;  
Best Local Similarity 85.3%; Pred. No. 2.6e-163;  
Matches 814; Conservative 0; Mismatches 115; Indels 25; Gaps 2;

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Qy      3977 TCCTCCTCCTCTCCTCTGGTCCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACA 4036
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Db      121 TCCTCCTCCTCTCCTCTGGTCCCTGGGCACCCTGGAGGAAGTGCTGCTGAGTCAGCA 180

Qy      4037 GATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGA 4096
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Db      181 GGTCTCCCCAGAGTCCTCAGGGAGCCTCTGCCTTACCACTACCATCAGCTTCACTTGC 240

Qy      4097 CAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGT 4156
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Db      241 TGGAGGCAACCCAATGAGGGTTCCAGCAGCCAAGAAGAGGAGGGGCCAAGCACCTCGCCT 300

Qy      4157 ATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTT 4216
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Db      301 GACGCAGAGTCCTTGTTCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGCTCATTTT 360

Qy      4217 CTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTC 4276
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Qy      4277 ATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGACAG 4336
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Db      421 ATCAAAAATTACAAGCGCTGCTTTCTGTGATCTTCGGCAAAGCCTCCGAGTCCCTGAAG 480
Qy      4337 CTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGTC 4396
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Db      481 ATGATCTTTGGCATTGACGTGAAGGAAGTGACCCCGCCAGCAACACCTACACCCTTGTC 540
Qy      4397 ACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACA 4456
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Db      541 ACCTGCCTGGGCCTTTCTATGATGGCCTGCTGGGTAATAATCAGATCTTTCCCAAGACA 600
Qy      4457 GGCTTCCTGATAATTGTCTTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAG 4516
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Db      601 GGCTTCCTGATAATCGTCTTGGGCACAATTGCAATGGAGGGCGACAGCGCCTCTGAGGAG 660
Qy      4517 GAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTAT 4576
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Db      661 GAAATCTGGGAGGAGCTGGGTGTGATGGGGTGTATGATGGGAGGGAGCACACTGTCTAT 720
Qy      4577 GGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGG 4635
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Db      721 GGGGAGCCCAGGAAACTGCTCACCCAAGATTGGGTGCAGGAAAAGTACCTGGAGTACCGG 780
Qy      4636 CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT 4695
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Db      781 CAGGTACCCGGCAGTAATCCTGCGCGCTATGAGTTCCTGTGGGGTCCAAGGGCTCTGGCT 840
Qy      4696 GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT 4755
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Db      841 GAAACCAGCTATGTGAAAGTCCTGGAGCATGTGGTCAGGGTCAATGCAAGAGTTCGCATT 900
Qy      4756 TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGA 4809
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Db      901 GCCTACCCATCCCTGCGTGAAGCAGCTTTGTTAGAGGAGGAAGAGGGAGTCTGA 954

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#### RESULT 14

DQ034795

LOCUS DQ034795 1008 bp DNA linear GSS 02-JUN-2005

DEFINITION Homo sapiens MAGEA3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION DQ034795

VERSION DQ034795.1 GI:66886004

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1008)

AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees

JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)

PUBMED 15869325

REFERENCE 2 (bases 1 to 1008)

AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment. Translation starts at the beginning of  
alignment.

FEATURES Location/Qualifiers  
source 1..1008  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
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/chromosome="X"  
gene <1..>1008  
/gene="MAGEA3"  
/locus\_tag="HC4231"

ORIGIN

Query Match 12.0%; Score 678.4; DB 14; Length 1008;  
Best Local Similarity 81.3%; Pred. No. 6.9e-158;  
Matches 820; Conservative 0; Mismatches 166; Indels 22; Gaps 2;

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Qy      3878 ATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAA 3937
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Db      61 ATCATGCCTCTTGAGCAGAGGAGTCACTGCAAGCCTGAAGAAGGCCTTGAGGCCCGA 120

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Db      121 GGAGAGGCCCTGGGCCTGGTGGGTGCGCAGGCTCCTGCTACTGAGGAGCAGGAGGCTGCC 180

Qy      3977 TCCTCCTCCTCCTCCTCTGGTCCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACA 4036
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Db      181 TCCTCCTCTTCTACTCTAGTTGAAGTCACCTTGGGGGAGGTGCCTGCTGCCGAGTCACCA 240

Qy      4037 GATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGA 4096
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Db      241 GATCCTCCCCAGAGTCCTCAGGGAGCCTCCAGCCTCCCCACTACCATGAACACCTCTC 300

Qy      4097 CAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGT 4156
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Db      301 TGGAGCCAATCCTATGAGGACTCCAGCAACCAAGAAGAGGAGGGGCCAAGCACCTTCCCT 360

Qy      4157 ATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTT 4216
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Db      361 GACCTGGAGTCTGAGTTCCAAGCAGCACTCAGTAGGAAGGTGGCCGAGTTGGTTTCATTTT 420

Qy      4217 CTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTC 4276
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Db      421 CTGCTCCTCAAGTATCGAGCCAGGGAGCCGGTCACAAAGGCAGAAATGCTGGGGAGTGTC 480

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Db      481 GTCGGAAATTGGCAGTATTTCTTTCTGTGATCTTCAGCAAAGCTTCCAGTTCTTGCA 540

Qy      4337 CTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCAACGGCCACTCCTATGTCCTTGTC 4396
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Db      541 CTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACTTGTACATCTTTGCC 600

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Db      601  ACCTGCCTGGGCCTCTCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAAGGCA 660
Qy      4457 GGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAG 4516
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Db      661  GGCTTCCTGATAATCGTCCTGGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 720
Qy      4517 GAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTAT 4576
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Qy      4577 GGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGG 4635
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Db      781  GGGGATCCCAAGAAGCTGCTCACCCAACATTTCTGTCAGGAAAAGTACCTGGAGTACCGG 840
Qy      4636 CAGGTGCCCGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT 4695
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Db      841  CAGGTCCCGGACAGTGATCCTGCATGTTATGAATTCCTGTGGGGTCCAAGGGCCCTCGTT 900
Qy      4696 GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT 4755
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Db      901  GAAACCAGCTATGTGAAAGTCCTGCACCATATGGTAAAGATCAGTGGAGGACCTCACATT 960
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#### RESULT 15

BQ224380

LOCUS BQ224380 811 bp mRNA linear EST 02-MAY-2002

DEFINITION AGENCOURT\_7549013 NIH\_MGC\_68 Homo sapiens cDNA clone IMAGE:6059308  
5', mRNA sequence.

ACCESSION BQ224380

VERSION BQ224380.1 GI:20405780

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 811)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: DCTD/DTP/Gazdar

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM13325 row: m column: 05

High quality sequence stop: 591.

#### FEATURES

source

Location/Qualifiers

1. .811

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/mol\_type="mRNA"

/db\_xref="taxon:9606"

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/clone_lib="NIH_MGC_68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies. "

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# ORIGIN

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Query Match          11.9%; Score 675.8; DB 3; Length 811;
Best Local Similarity 97.4%; Pred. No. 2.9e-157;
Matches 708; Conservative 0; Mismatches 17; Indels 2; Gaps 2;

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Qy      3936 AACAAAGAGGCCCTGGGCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCTCTCTCTGG 3995
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Qy 4534 GAGTGTG 4540  
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Job time : 24236 secs

SCORE 1.3 BuildDate: 12/06/2005

# SCORE Search Results Details for Application 08819669 and Search Result us-08-819-669e- 26.rag.

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<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

This page gives you Search Results detail for the Application 08819669 and Search Result us-08-819-669e-26.rag.

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 25, 2006, 00:50:36 ; Search time 196 Seconds  
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20.995 Million cell updates/sec

Title: US-08-819-669E-26  
Perfect score: 52  
Sequence: 1 EADPTGHSY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: geneseqpl990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	52	100.0	9	2	AAR29769	Aar29769 Antigen E
2	52	100.0	9	2	AAR63675	Aar63675 Synthetic
3	52	100.0	9	2	AAR50281	Aar50281 MAGE-1 no
4	52	100.0	9	2	AAY38303	Aay38303 MAGE-deri
5	52	100.0	9	2	AAR47330	Aar47330 HLA-A1 MA
6	52	100.0	9	2	AAR49224	Aar49224 HLA-A1 MA
7	52	100.0	9	2	AAR78824	Aar78824 MAGE-1 cy
8	52	100.0	9	2	AAR82988	Aar82988 P815 anti
9	52	100.0	9	2	AAR83932	Aar83932 MHC class
10	52	100.0	9	2	AAR65112	Aar65112 MAGE 1 im
11	52	100.0	9	2	AAR65135	Aar65135 MAGE 1 im
12	52	100.0	9	2	AAR75954	Aar75954 Melanoma
13	52	100.0	9	2	AAR99343	Aar99343 MAGE-1 no
14	52	100.0	9	2	AAR90692	Aar90692 Human leu
15	52	100.0	9	2	AAW00897	Aaw00897 Human mel
16	52	100.0	9	2	AAW54622	Aaw54622 Peptide f
17	52	100.0	9	2	AAW78838	Aaw78838 MAGE-1 pr
18	52	100.0	9	2	AAW77125	Aaw77125 gp75/TRP-
19	52	100.0	9	2	AAW68371	Aaw68371 Human MAG
20	52	100.0	9	2	AAW75734	Aaw75734 Peptidase
21	52	100.0	9	2	AAW75736	Aaw75736 Peptidase
22	52	100.0	9	2	AAY02137	Aay02137 Peptide u
23	52	100.0	9	2	AAW56729	Aaw56729 MAGE-1 an
24	52	100.0	9	2	AAW98945	Aaw98945 HLA-A1 bi
25	52	100.0	9	2	AAY10424	Aay10424 HLA Class
26	52	100.0	9	2	AAY10623	Aay10623 Peptide a
27	52	100.0	9	2	AAY10633	Aay10633 Peptide a
28	52	100.0	9	2	AAY40228	Aay40228 Amino aci
29	52	100.0	9	2	AAY45884	Aay45884 Immunogen
30	52	100.0	9	2	AAY46334	Aay46334 Immunogen
31	52	100.0	9	2	AAY33147	Aay33147 Human MAG
32	52	100.0	9	2	AAY25177	Aay25177 MAGE-1 pe
33	52	100.0	9	2	AAY23250	Aay23250 Peptide d
34	52	100.0	9	2	AAY53541	Aay53541 Human MAG
35	52	100.0	9	2	AAY26884	Aay26884 Tumour-de
36	52	100.0	9	2	AAY22126	Aay22126 Tumour re
37	52	100.0	9	2	AAY00685	Aay00685 Tumour an
38	52	100.0	9	2	AAY49637	Aay49637 Tumour an
39	52	100.0	9	2	AAY01727	Aay01727 Exemplary
40	52	100.0	9	3	AAY71494	Aay71494 Human MAG
41	52	100.0	9	3	AAY90778	Aay90778 Human leu
42	52	100.0	9	3	AAB13741	Aab13741 Peptide f
43	52	100.0	9	3	AAY96509	Aay96509 MAGE-1 no
44	52	100.0	9	3	AAB33650	Aab33650 MHC class
45	52	100.0	9	3	AAB23659	Aab23659 Cytotoxic

#### ALIGNMENTS

RESULT 1  
 AAR29769  
 ID AAR29769 standard; peptide; 9 AA.  
 XX  
 AC AAR29769;  
 XX  
 DT 25-MAR-2003 (revised)

DT 22-APR-1993 (first entry)  
 XX  
 DE Antigen E peptide.  
 XX  
 KW Antigen; tumorigenic cell; A+ B+; T-cell; response; syngeneic; animal;  
 KW mouse; tumour rejection antigen precursor; TRAP; PlA.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09220356-A1.  
 XX  
 PD 26-NOV-1992.  
 XX  
 PF 22-MAY-1992; 92WO-US004354.  
 XX  
 PR 23-MAY-1991; 91US-00705702.  
 PR 09-JUL-1991; 91US-00728838.  
 PR 23-SEP-1991; 91US-00764364.  
 PR 12-DEC-1991; 91US-00807043.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Boon T, Van Der Bruggen P, Van Den Eynde B, Van Pel A, De Plaen E;  
 PI Lurquin C, Chomez P, Traversari C;  
 XX  
 DR WPI; 1992-415460/50.  
 XX  
 PT Nucleic acid mol. encoding a human tumour rejection antigen precursor -  
 PT useful as an immunostimulant in a vaccine for treating and preventing  
 PT cancers, also useful in diagnosis.  
 XX  
 PS Disclosure; Page 97; 142pp; English.  
 XX  
 CC This sequence represents the sequence of the antigen E. Antigens such as  
 CC this one cause a T-cell response to be elicited which transplanted into a  
 CC syngeneic animal; usually a mouse. This antigen is derived from the cell  
 CC line MEL3.1. See also AAQ32351. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EADPTGHSY 9  
 |||||  
 Db 1 EADPTGHSY 9

RESULT 2  
 AAR63675

ID AAR63675 standard; protein; 9 AA.  
 XX  
 AC AAR63675;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 22-JUN-1995 (first entry)  
 XX  
 DE Synthetic peptide derived from exon 3.1 of MAGE 1.  
 XX

KW Melanoma antigen-1; MAGE-1; cytolytic T cells; antigen E; exon 3.1.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9423031-A1.  
 XX  
 PD 13-OCT-1994.  
 XX  
 PF 17-MAR-1994; 94WO-US002877.  
 XX  
 PR 26-MAR-1993; 93US-00037230.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Gaugler B, Van Den Eynde B, Boon-Falleur T, Van Der Bruggen P;  
 XX  
 DR WPI; 1994-333192/41.  
 XX  
 PT New tumour rejection antigen precursor MAGE3 - useful in treatment and  
 PT diagnosis of cancer.  
 XX  
 PS Example 34; Page 36; 105pp; English.  
 XX  
 CC AAR63675 is a synthetic peptide derived from exon 3.1 of melanoma antigen  
 CC -1 (MAGE-1), it was used to transfer antigen-E cytolytic T lymphocyte  
 CC sensitivity to normally non-sensitive cells. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
 |||||  
 Db 1 EADPTGHSY 9

# RESULT 3

AAR50281

ID AAR50281 standard; protein; 9 AA.

XX

AC AAR50281;

XX

DT 25-MAR-2003 (revised)

DT 26-SEP-1994 (first entry)

XX

DE MAGE-1 nonapeptide.

XX

KW MAGE; nonapeptide; cancer; melanoma; breast cancer; HLA;

KW histocompatibility; human leucocyte antigen; probe; treatment; therapy;

KW vaccine.

XX

OS Synthetic.

XX

PN WO9405304-A1.

XX

PD 17-MAR-1994.

XX

PF 30-AUG-1993; 93WO-US008157.

XX  
 PR 31-AUG-1992; 92US-00938334.  
 PR 26-MAR-1993; 93US-00037230.  
 PR 07-JUN-1993; 93US-00073103.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Boon-Falleur T, Van Der Bruggen P, De Plaen E, Lurquin C;  
 PI Traversari C;  
 XX  
 DR WPI; 1994-100844/12.  
 DR N-PSDB; AAQ44751.  
 XX  
 PT New nona:peptide derived from tumour rejection antigen precursor -  
 PT presented by HLA-A1 cancer cells, for use in diagnosis or therapy of esp.  
 PT melanoma and breast cancer.  
 XX  
 PS Disclosure; Page 19; 33pp; English.  
 XX  
 CC An isolated nonapeptide having the amino acid sequence Glu-Val-Asp- Pro-  
 CC Ile-Gly-His-Leu-Tyr is derived from the tumour rejection antigen  
 CC precursor encoded by the MAGE-3 gene and presented by HLA-A1. The  
 CC nonapeptide can be used in a vaccine to treat a cancerous condition  
 CC involving HLA-A1 subtype cancerous cells. The nucleic acid encoding the  
 CC nonapeptide can be used as a probe to identify tumour cells. This  
 CC sequence is homologous to the peptide described and is encoded by the  
 CC MAGE-1 gene. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25  
 CC -MAR-2003 to correct PI field.)  
 XX  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
 |||||  
 Db 1 EADPTGHSY 9

RESULT 4  
 AAY38303  
 ID AAY38303 standard; peptide; 9 AA.  
 XX  
 AC AAY38303;  
 XX  
 DT 29-SEP-1999 (first entry)  
 XX  
 DE MAGE-derived HLA-binding peptide.  
 XX  
 KW Immunogen; HLA; human leukocyte antigen; binding motif; antiviral; MHC;  
 KW major histocompatibility complex; viral infection; anticancer;  
 KW prostate cancer; lymphoma; hepatitis; AIDS; diagnostic; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9403205-A1.  
 XX  
 PD 17-FEB-1994.  
 XX  
 PF 06-AUG-1993; 93WO-US007421.



XX  
 PR 07-AUG-1992; 92US-00926666.  
 PR 05-MAR-1993; 93US-00027746.  
 XX  
 PA (CYTE-) CYTEL CORP.  
 XX  
 PI Kubo RT, Grey HM, Sette A, Celis E;  
 XX  
 DR WPI; 1994-065403/08.  
 XX  
 PT Peptide which specifically binds selected MHC allele - used to induce an  
 PT immune response for treatment or prevention of viral infection or cancer,  
 PT or for diagnosis.  
 XX  
 PS Disclosure; Page 112; 150pp; English.  
 XX  
 CC The sequence is a specific example of a group of new immunogenic peptides  
 CC having an HLA-A3.2, HLA-A1, HLA-A11 or HLA-A24.1 binding motif. For  
 CC example, the peptides having an HLA-A3.2 binding motif each have 9-10  
 CC residues and contain, from the N-terminus to the C-terminus, (a) a first  
 CC conserved residue selected from L, M, I, V, S, A, T, F, C, G, D and E and  
 CC (b) a second conserved residue of K, R, Y, H or F, where the first and  
 CC second conserved residues are separated by 6-7 residues. The peptides are  
 CC capable of binding selected MHC molecules and inducing an immune  
 CC response. They can be used to treat and/or prevent viral infection and  
 CC cancer, e.g. prostate cancer, lymphoma, hepatitis or AIDS. They can also  
 CC be used to produce antibodies for use as diagnostic or therapeutic  
 CC agents. The peptides can also be used as diagnostic agents  
 XX  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
 |||||  
 Db 1 EADPTGHSY 9

# RESULT 5

AAR47330

ID AAR47330 standard; protein; 9 AA.

XX

AC AAR47330;

XX

DT 14-MAY-2003 (revised)

DT 25-MAR-2003 (revised)

DT 31-AUG-1994 (first entry)

XX

DE HLA-A1 MAGE 1 antigen peptide fragment 161-169.

XX

KW Immunogenic; HLA-A3.2; HLA-A1; HLA-A11; binding motif; MHC molecule;

KW immune response; viral infection; cancer; prostate cancer; lymphoma;

KW hepatitis; AIDS; antibody; diagnosis; melanoma antigen.

XX

OS Synthetic.

XX

PN WO9403205-A1.

XX

PD 17-FEB-1994.

```

XX
PF 06-AUG-1993; 93WO-US007421.
XX
PR 07-AUG-1992; 92US-00926666.
PR 05-MAR-1993; 93US-00027746.
XX
PA (CYTE-) CYTEL CORP.
XX
PI Kubo RT, Grey HM, Sette A, Celis E;
XX
DR WPI; 1994-065403/08.
XX
PT Peptide which specifically binds selected MHC allele - used to induce an
PT immune response for treatment or prevention of viral infection or cancer,
PT or for diagnosis.
XX
PS Example 8; Page 52; 150pp; English.
XX
CC The sequences given in AAR47304-33 and AAR49201-44 are immunogenic
CC peptides which have a HLA-A3.2, HLA-A1 or a HLA-A11 binding motif. These
CC peptides may be used in the composition of the invention. These peptides
CC are capable of binding selected MHC molecules and inducing an immune
CC response. They can be used to treat and/or prevent viral infection and
CC cancer, eg. prostate cancer, lymphoma, hepatitis or AIDS. They can also
CC be used to produce antibodies for use as diagnostic or therapeutic
CC agents. The peptides can also be used as diagnostic agents. (Updated on
CC 25-MAR-2003 to correct PN field.) (Updated on 14-MAY-2003 to correct PS
CC field.)
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
   |||||
Db 1 EADPTGHSY 9

RESULT 6
AAR49224
ID AAR49224 standard; protein; 9 AA.
XX
AC AAR49224;
XX
DT 14-MAY-2003 (revised)
DT 25-MAR-2003 (revised)
DT 31-AUG-1994 (first entry)
XX
DE HLA-A1 MAGE 1 antigen peptide fragment 958.01.
XX
KW Immunogenic; HLA-A3.2; HLA-A1; HLA-A11; binding motif; MHC molecule;
KW immune response; viral infection; cancer; prostate cancer; lymphoma;
KW hepatitis; AIDS; antibody; diagnosis; melanoma antigen.
XX
OS Synthetic.
XX
PN W09403205-A1.
XX
PD 17-FEB-1994.

```

```

XX
PF 06-AUG-1993; 93WO-US007421.
XX
PR 07-AUG-1992; 92US-00926666.
PR 05-MAR-1993; 93US-00027746.
XX
PA (CYTE-) CYTEL CORP.
XX
PI Kubo RT, Grey HM, Sette A, Celis E;
XX
DR WPI; 1994-065403/08.
XX
PT Peptide which specifically binds selected MHC allele - used to induce an
PT immune response for treatment or prevention of viral infection or cancer,
PT or for diagnosis.
XX
PS Example 16; Page 116; 150pp; English.
XX
CC The sequences given in AAR47304-33 and AAR49201-44 are immunogenic
CC peptides which have a HLA-A3.2, HLA-A1 or a HLA-A11 binding motif. These
CC peptides may be used in the composition of the invention. These peptides
CC are capable of binding selected MHC molecules and inducing an immune
CC response. They can be used to treat and/or prevent viral infection and
CC cancer, eg. prostate cancer, lymphoma, hepatitis or AIDS. They can also
CC be used to produce antibodies for use as diagnostic or therapeutic
CC agents. The peptides can also be used as diagnostic agents. (Updated on
CC 25-MAR-2003 to correct PN field.) (Updated on 14-MAY-2003 to correct PS
CC field.)
XX
SQ Sequence 9 AA;

Query Match          100.0%; Score 52; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

RESULT 7
AAR78824
ID AAR78824 standard; peptide; 9 AA.
XX
AC AAR78824;
XX
DT 26-MAR-1996 (first entry)
XX
DE MAGE-1 cytotoxic T lymphocyte epitope.
XX
KW MAGE-1; cytotoxic T; CTL; epitope; helper T; HTL; lymphocyte; cell;
KW viruses; parasites; tumours; antigens; disease prevention; treatment.
XX
OS Homo sapiens.
XX
PN WO9522317-A1.
XX
PD 24-AUG-1995.
XX
PF 16-FEB-1995; 95WO-US002121.
XX

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PR 16-FEB-1994; 94US-00197484.  
 XX  
 PA (CYTE-) CYTEL CORP.  
 XX  
 PI Vitiello MA, Chesnut RW, Sette AD, Celis E, Grey H;  
 XX  
 DR WPI; 1995-302545/39.  
 XX  
 PT Compsn. inducing cytotoxic T lymphocyte response to pref. viral,  
 PT bacterial, parasitic or tumour antigens - useful in the treatment and  
 PT prevention of diseases associated with the antigen e.g. hepatitis B.  
 XX  
 PS Disclosure; Page 17; 109pp; English.  
 XX  
 CC A compsn. which induces a cytotoxic T lymphocyte (CTL) response to an  
 CC antigen (Ag) in a mammal comprises, a CTL Ag response inducing peptide  
 CC (i.e. AAR78824-R78853) and a lipid conjugated helper T cell inducing  
 CC peptide. The compsn. induces a CTL response to bacterial, viral or tumour  
 CC Ags, and is therefore useful in the treatment and prevention of diseases  
 CC associated with the Ag  
 XX  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
 |||||  
 Db 1 EADPTGHSY 9

RESULT 8  
 AAR82988  
 ID AAR82988 standard; peptide; 9 AA.  
 XX  
 AC AAR82988;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 26-FEB-1996 (first entry)  
 XX  
 DE P815 antigenic peptide.  
 XX  
 KW P815 antigen; P1A antigen; cancer; vaccine.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9523874-A1.  
 XX  
 PD 08-SEP-1995.  
 XX  
 PF 23-FEB-1995; 95WO-US002203.  
 XX  
 PR 01-MAR-1994; 94US-00204727.  
 PR 10-MAR-1994; 94US-00209172.  
 PR 01-SEP-1994; 94US-00299849.  
 PR 30-NOV-1994; 94US-00346774.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI De Plaen E, Boon-Falleur T, Lethe B, Szikora J, De Smet C;

PI Chomez P, Gaugler B, Van Den Eynde B, Brasseur F, Patard J;  
 PI Weynants P, Marchand M, Van Der Bruggen P;  
 XX  
 DR WPI; 1995-320586/41.  
 XX  
 PT Determn. of cancerous condition(s) - using a nucleic acid as a primer to  
 PT determine expression of a MAGE tumour rejection antigen precursor.  
 XX  
 PS Example 13; Page 22; 121pp; English.  
 XX  
 CC Using the sequence of the P815A antigen precursor gene P1A (AAT01176), an  
 CC antigenic peptide (AAR82988) which was A+B+ (i.e. characteristic of cells  
 CC which express both A and B antigens) was produced. The peptide lysed  
 CC PO.HTR cells in the presence of cytolytic T lymphocyte cell lines, and  
 CC may be useful as a vaccine component. (Updated on 25-MAR-2003 to correct  
 CC PI field.)  
 XX  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
 |||||  
 Db 1 EADPTGHSY 9

RESULT 9  
 AAR83932  
 ID AAR83932 standard; peptide; 9 AA.  
 XX  
 AC AAR83932;  
 XX  
 DT 05-JUN-1996 (first entry)  
 XX  
 DE MHC class I restricted antigenic peptide #2.  
 XX  
 KW MHC class I; antigen; MAGE; melanoma; breast cancer; bladder cancer;  
 KW Titermax; cytotoxic T-lymphocyte; tumour; pathogenic disease; bacteria;  
 KW parasite; human; animal.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9528958-A1.  
 XX  
 PD 02-NOV-1995.  
 XX  
 PF 21-APR-1995; 95WO-US004975.  
 XX  
 PR 22-APR-1994; 94US-00233496.  
 XX  
 PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
 XX  
 PI Nikolic-Zugic J, Dyall R;  
 XX  
 DR WPI; 1995-382848/49.  
 XX  
 PT Cytotoxic T-cell induction by MHC class I-restricted peptide in adjuvant  
 PT - useful for treating tumours and bacterial or parasitic pathogenic  
 PT diseases.

XX  
 PS Claim 11; Page 38; 50pp; English.  
 XX  
 CC The sequences given in AAR83931-49 are MHC class I restricted 8-12 amino  
 CC acid antigenic peptides. This peptide is derived from MAGE and is present  
 CC in melanoma, breast and bladder cancer. These peptides may be  
 CC administered to a subject in combination with a suitable adjuvant, pref.  
 CC Titermax (RTM), to induce cytotoxic T- lymphocytes. This method may be  
 CC used in the treatment of a tumour or a pathogenic disease, esp. diseases  
 CC of bacterial or parasitic origin, in humans and animals, e.g monkeys,  
 CC dogs cows, horses, etc  
 XX  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
 |||||  
 Db 1 EADPTGHSY 9

# RESULT 10

AAR65112

ID AAR65112 standard; peptide; 9 AA.

XX

AC AAR65112;

XX

DT 25-MAR-2003 (revised)

DT 06-OCT-1995 (first entry)

XX

DE MAGE 1 immunogenic peptide 161-169.

XX

KW MAGE 1; immunogenic peptide 161-169; cytotoxic C cells;

KW in vitro activation; cancer; AIDS; bacterial infections; malaria;

KW fungal infections; tuberculosis; hepatitis.

XX

OS Homo sapiens.

XX

PN WO9504817-A1.

XX

PD 16-FEB-1995.

XX

PF 01-AUG-1994; 94WO-US008672.

XX

PR 06-AUG-1993; 93US-00103401.

XX

PA (CYTE-) CYTEL CORP.

XX

PI Celis E, Kubo R, Serra H, Tsai V, Wentworth P;

XX

DR WPI; 1995-090895/12.

XX

PT In vitro activation of cytotoxic T cells for selected killing of target  
 PT cells - for treating e.g. cancer, AIDS, hepatitis etc.by incubating them  
 PT with antigen presenting cells loaded with appropriate immunogenic  
 PT peptide.

XX

PS Example 3; Page 35; 53pp; English.

XX

CC AAR65109-R65145 are immunogenic peptides, they are used in a new method  
CC for the in vitro activation of cytotoxic T cells (CTC). This is achieved  
CC by incubating the CTCs with antigen presenting cells loaded with an  
CC appropriate immunogenic peptide (e.g. one of the above peptides). By  
CC selecting the peptides used the following diseases and infections can be  
CC treated; cancer, AIDS, hepatitis, other viral and bacterial infections,  
CC malaria and tuberculosis. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9

|||||||

Db 1 EADPTGHSY 9

#### RESULT 11

AAR65135

ID AAR65135 standard; peptide; 9 AA.

XX

AC AAR65135;

XX

DT 25-MAR-2003 (revised)

DT 09-OCT-1995 (first entry)

XX

DE MAGE 1 immunogenic peptide A01.

XX

KW MAGE 1; immunogenic peptide A01; cytotoxic C cells; in vitro activation;

KW cancer; AIDS; bacterial infections; malaria; fungal infections;

KW tuberculosis; hepatitis.

XX

OS Homo sapiens.

XX

PN WO9504817-A1.

XX

PD 16-FEB-1995.

XX

PF 01-AUG-1994; 94WO-US008672.

XX

PR 06-AUG-1993; 93US-00103401.

XX

PA (CYTE-) CYTEL CORP.

XX

PI Celis E, Kubo R, Serra H, Tsai V, Wentworth P;

XX

DR WPI; 1995-090895/12.

XX

PT In vitro activation of cytotoxic T cells for selected killing of target  
PT cells - for treating e.g. cancer, AIDS, hepatitis etc.by incubating them  
PT with antigen presenting cells loaded with appropriate immunogenic  
PT peptide.

XX

PS Example 3; Page 38; 53pp; English.

XX

CC AAR65109-R65145 are immunogenic peptides, they are used in a new method  
CC for the in vitro activation of cytotoxic T cells (CTC). This is achieved  
CC by incubating the CTCs with antigen presenting cells loaded with an  
CC appropriate immunogenic peptide (e.g. one of the above peptides). By

CC selecting the peptides used the following diseases and infections can be  
CC treated; cancer, AIDS, hepatitis, other viral and bacterial infections,  
CC malaria and tuberculosis. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| | | | | | | |  
Db 1 EADPTGHSY 9

RESULT 12

AAR75954

ID AAR75954 standard; peptide; 9 AA.

XX

AC AAR75954;

XX

DT 06-MAR-1996 (first entry)

XX

DE Melanoma antigen (MAGE-1) epitope.

XX

KW MAGE-3; melanoma antigen; vaccine; immune response; immunogenic peptide;

KW cytotoxic T lymphocyte response; CTL; melanoma; breast cancer; antibody.

XX

OS Homo sapiens.

XX

PN WO9519783-A1.

XX

PD 27-JUL-1995.

XX

PF 25-JAN-1995; 95WO-US001000.

XX

PR 25-JAN-1994; 94US-00186266.

XX

PA (CYTE-) CYTEL CORP.

XX

PI Kubo RT, Grey HM, Sette A, Celis E;

XX

DR WPI; 1995-269270/35.

XX

PT Immunogenic peptide(s) that induce immune response to cancer cells - that

PT express a MAGE-3 protein peptide epitope used in vaccines or adoptive

PT immuno:therapy to induce cytotoxic T lymphocytes.

XX

PS Example; Page 33; 44pp; English.

XX

CC AAR75954 is derived from MAGE-1 protein. It was used to show the

CC specificity of CTL response to MAGE-3 peptides shown in AAR75942-53.

CC AAR75942 is derived from the sequence of the melanoma antigen (MAGE-3)

CC protein and can be used to elicit a primary cytotoxic T lymphocyte

CC response against cells expressing MAGE-3. Synthetic peptides AAR75945-53

CC can be used therapeutically to elicit CTL responses to melanoma, breast,

CC colon, prostate, or other cells which express proteins with this epitope.

CC The peptides have specific HLA-A1 binding capacity

XX

SQ Sequence 9 AA;



Query Match 100.0%; Score 52; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
|||||||  
Db 1 EADPTGHSY 9

RESULT 13

AAR99343

ID AAR99343 standard; protein; 9 AA.

XX

AC AAR99343;

XX

DT 22-APR-1997 (first entry)

XX

DE MAGE-1 nonapeptide.

XX

KW HLA binding peptide; cell lysis; cytolytic T cell; MAGE family; human;

KW tumour rejection antigen precursor; TRA; MAGE-1; tumour; cancer cell;

KW antibody; melanoma; universal effector cell; vaccine; breast cancer; CTL;

KW therapy.

XX

OS Homo sapiens.

XX

PN WO9626214-A1.

XX

PD 29-AUG-1996.

XX

PF 01-FEB-1996; 96WO-US001489.

XX

PR 23-FEB-1995; 95US-00393273.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Boon-Falleur T, Van Der Bruggen P, De Plaen E, Lurquin C;

PI Gaugler B, Van Den Eynde B, Traversari C, Romero P;

XX

DR WPI; 1996-402317/40.

DR N-PSDB; AAT35408.

XX

PT New nona:peptide(s) that bind to HLA molecule(s) and induce lysis - by  
PT specific cytolytic T cells, for diagnosis and treatment of tumours and to  
PT expand T cells in vitro.

XX

PS Example 4; Fig 4; 41pp; English.

XX

CC AAR99343-R99350 represent MAGE nonapeptides, based on the tumour  
CC rejection antigen region of the full length MAGE sequences. These  
CC peptides were used to design the nonapeptides of the invention (see  
CC AAR99337-R99342), which bind to a HLA molecule on a cell, and provoke  
CC lysis by cytolytic T cells (CTLs) specific for a complex of the HLA  
CC molecule and nonapeptide. The nonapeptides can be used diagnostically to  
CC identify tumours expressing a particular HLA molecule, or to identify  
CC cancer cells. The peptides can also be used therapeutically, to induce a  
CC CTL response to tumours (where the peptides are optionally coupled to  
CC tumour-specific antibodies), or to induce a response by CTLs that are  
CC otherwise inactive. The peptide sequences may also be used to expand  
CC specific CTLs in vitro for later return to the patient, such as for  
CC treating melanoma. Tumour cells can be identified by using DNA encoding

CC the nonapeptides as probes. Non-human cells transformed with the HLA-A1  
CC gene and a DNA sequence encoding one of the peptides, can be used to  
CC generate CTLs, or to detect the presence of CTLs in human samples. The  
CC non-human transformed cells, when polytransformed, are universal effector  
CC cells, and can be used in vaccines, or for treating melanoma or breast  
CC cancer

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| | | | | | | |  
Db 1 EADPTGHSY 9

RESULT 14

AAR90692

ID AAR90692 standard; peptide; 9 AA.

XX

AC AAR90692;

XX

DT 31-JUL-1996 (first entry)

XX

DE Human leukocyte antigen (HLA-A1) presented peptide MZ2-E.

XX

KW Human leukocyte antigen; HLA-A1; MAGE-1 derived; blood mononuclear cell;

KW BMC; CD8-beta+ cell; cytolytic T cell; CTL cell; treatment; tumour cell;

KW diagnosis; assay; presented peptide.

XX

OS Synthetic.

XX

PN WO9535500-A1.

XX

PD 28-DEC-1995.

XX

PF 14-JUN-1995; 95WO-US007559.

XX

PR 17-JUN-1994; 94US-00261541.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Coulie P, Van Der Bruggen P, Boon-Falleur T;

XX

DR WPI; 1996-058510/06.

XX

PT Prodn. of specific cytolytic T cell sub-populations - by contacting blood

PT mononuclear cells with specific peptide(s) and a population of CD8-

PT beta(+) cells.

XX

PS Claim 5; Page 19; 25pp; English.

XX

CC The present peptide is the human leukocyte antigen (HLA-A1), MAGE-1

CC derived presented peptide, MZ2-E. By contacting a sample of blood

CC mononuclear cells (BMC) with the peptide (which binds directly to HLA-A1

CC mols. on the surface of the BMC) and CD8-beta+ cells (which stimulate

CC peptide/HLA-A1 complex specific CD8-beta+ cells), a peptide/HLA-A1

CC complex specific cytolytic T (CTL) cell subpopulation can be obtd. . The

CC CTL cells obtd. can be administered to a patient to treat tumour cell

CC related conditions, and can be used in diagnostic methods, e.g. in assays  
CC for the peptide/HLA-A1 complex  
XX  
SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| | | | | | | |  
Db 1 EADPTGHSY 9

RESULT 15

AAW00897

ID AAW00897 standard; peptide; 9 AA.

XX

AC AAW00897;

XX

DT 23-MAY-1997 (first entry)

XX

DE Human melanoma MAGE1 tumour associated antigen p161-169.

XX

KW Adeno-associated virus; vector; liposome; transfection; dendritic cell;  
KW melanoma; MAGE1; adoptive immunotherapy; tumour associated antigen.

XX

OS Homo sapiens.

XX

PN WO9703703-A1.

XX

PD 06-FEB-1997.

XX

PF 19-JUL-1996; 96WO-US012012.

XX

PR 21-JUL-1995; 95US-0001312P.

PR 01-NOV-1995; 95US-0007184P.

PR 01-DEC-1995; 95US-00566286.

XX

PA (RHON ) RHONE POULENC RORER PHARM INC.

XX

PI Philip R, Lebkowski JS;

XX

DR WPI; 1997-145208/13.

XX

PT Adeno-associated virus:liposome complexes for transfecting dendritic  
PT cells - for inducing immune response, useful for treating e.g. neoplasia  
PT or infections.

XX

PS Example 5; Page 58; 134pp; English.

XX

CC Tumour associated antigens (AAW13660-61, AAW00878-903) can be loaded into  
CC dendritic cells and used to induce antitumour immunity. Alternatively,  
CC the dendritic cells are transfected with adeno associated virus plasmid  
CC DNA (which includes DNA encoding the tumour associated antigen) complexed  
CC with cationic liposomes. The antigen loaded or transfected dendritic  
CC cells can be used to generate tumour antigen-specific cytotoxic T  
CC lymphocytes for use in adoptive immunotherapy in a patient having the  
CC corresponding tumour. A suitable antigen comprises amino acids 161-169  
CC (AAW00897) of human melanoma MAGE1

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| | | | | | | |  
Db 1 EADPTGHSY 9

Search completed: August 25, 2006, 00:54:22  
Job time : 199 secs

SCORE 1.3 BuildDate: 12/06/2005
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<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

start

[Go Back to previous page](#)

OM protein - protein search, using sw model

Title: US-08-819-669E-26  
Perfect score: 52  
Sequence: 1 EADPTGHSY 9

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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6:  /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7:  /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
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1	52	100.0	9	1	US-07-938-334C-1	Sequence 1, Appli
2	52	100.0	9	1	US-08-073-103A-12	Sequence 12, Appl
3	52	100.0	9	1	US-08-299-849B-26	Sequence 26, Appl
4	52	100.0	9	1	US-08-186-266-1	Sequence 1, Appli
5	52	100.0	9	1	US-08-443-341-12	Sequence 12, Appl
6	52	100.0	9	1	US-08-787-547-49	Sequence 49, Appl
7	52	100.0	9	1	US-08-498-461-4	Sequence 4, Appli
8	52	100.0	9	1	US-08-902-516-21	Sequence 21, Appl
9	52	100.0	9	1	US-08-142-368A-26	Sequence 26, Appl
10	52	100.0	9	1	US-09-036-582-1	Sequence 1, Appli
11	52	100.0	9	1	US-08-986-234-1	Sequence 1, Appli
12	52	100.0	9	2	US-08-967-727-26	Sequence 26, Appl
13	52	100.0	9	2	US-08-354-679C-12	Sequence 12, Appl
14	52	100.0	9	2	US-08-159-339A-99	Sequence 99, Appl
15	52	100.0	9	2	US-08-795-733B-1	Sequence 1, Appli
16	52	100.0	9	2	US-09-183-931-29	Sequence 29, Appl
17	52	100.0	9	2	US-08-393-273E-12	Sequence 12, Appl
18	52	100.0	9	2	US-08-037-230D-26	Sequence 26, Appl
19	52	100.0	9	2	US-09-183-706-4	Sequence 4, Appli
20	52	100.0	9	2	US-09-162-934-1	Sequence 1, Appli
21	52	100.0	9	2	US-09-061-388-21	Sequence 21, Appl
22	52	100.0	9	2	US-09-166-448-45	Sequence 45, Appl
23	52	100.0	9	2	US-09-567-995-4	Sequence 4, Appli
24	52	100.0	9	2	US-09-099-543C-21	Sequence 21, Appl
25	52	100.0	9	2	US-08-443-580F-12	Sequence 12, Appl
26	52	100.0	9	2	US-09-705-160-29	Sequence 29, Appl
27	52	100.0	9	2	US-09-165-863-1	Sequence 1, Appli
28	52	100.0	9	2	US-08-197-484-1	Sequence 1, Appli
29	52	100.0	9	2	US-09-697-884-45	Sequence 45, Appl
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32	52	100.0	9	2	US-09-583-850-26	Sequence 26, Appl
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34	52	100.0	9	2	US-09-574-749B-1	Sequence 1, Appli
35	52	100.0	9	2	US-09-579-197-26	Sequence 26, Appl
36	52	100.0	9	2	US-09-341-982-88	Sequence 88, Appl
37	52	100.0	9	2	US-09-404-026-26	Sequence 26, Appl
38	52	100.0	9	2	US-09-312-464-26	Sequence 26, Appl
39	52	100.0	9	2	US-09-318-141-1	Sequence 1, Appli
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41	52	100.0	9	2	US-09-000-003A-24	Sequence 24, Appl
42	52	100.0	9	2	US-09-169-717E-7	Sequence 7, Appli
43	52	100.0	9	2	US-09-601-729-131	Sequence 131, App
44	52	100.0	9	2	US-09-812-528-1	Sequence 1, Appli
45	52	100.0	9	2	US-09-806-769-1	Sequence 1, Appli

#### ALIGNMENTS

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RESULT 1
US-07-938-334C-1
; Sequence 1, Application US/07938334C
; Patent No. 5405940
; GENERAL INFORMATION:
;   APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
;   APPLICANT: De Plaen, Etienne; Lurquin Christophe; Traversari, Catia
;   TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
;   TITLE OF INVENTION: MAGE GENES AND USES THEREOF
;   NUMBER OF SEQUENCES: 22

```

```

;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Felfe & Lynch
;   STREET:    805 Third Avenue
;   CITY:     New York City
;   STATE:    New York
;   COUNTRY:   USA
;   ZIP:      10022
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;   COMPUTER:    IBM PS/2
;   OPERATING SYSTEM:  PC-DOS
;   SOFTWARE:    Wordperfect
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/07/938,334C
;   FILING DATE:    31-AUG-1992
;   CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;   NAME:    Hanson, No. 5405940man D.
;   REGISTRATION NUMBER:  30,946
;   REFERENCE/DOCKET NUMBER:  LUD 293
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (212) 688-9200
;   TELEFAX:   (212) 838-3884
;   INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:   9 amino acid residues
;   TYPE:     amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE:  protein
;   FEATURE:
;   NAME/KEY:  MAGE-1 derived nonapeptide
US-07-938-334C-1

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Query Match          100.0%;  Score 52;  DB 1;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 5e+05;
Matches      9;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

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Qy      1 EADPTGHSY 9
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Db      1 EADPTGHSY 9

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RESULT 2
US-08-073-103A-12
; Sequence 12, Application US/08073103A
; Patent No. 5462871
;   GENERAL INFORMATION:
;   APPLICANT:  Boon-Falleur, Thierry
;   APPLICANT:  van der Bruggen, Pierre
;   APPLICANT:  De Plaen, Etienne
;   APPLICANT:  Lurquin, Christophe
;   APPLICANT:  Traversari, Catia
;   APPLICANT:  Gaugler, Beatrice
;   APPLICANT:  Van den Eynde, Benoit
;   TITLE OF INVENTION:  ISOLATED NONAPEPTIDES DERIVED FROM
;   TITLE OF INVENTION:  MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THEREOF
;   NUMBER OF SEQUENCES:  22
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Felfe & Lynch
;   STREET:    805 Third Avenue
;   CITY:     New York City

```

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; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,103A
; FILING DATE: 7-JUNE-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,334
; FILING DATE: 31-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5462871man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5293.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-073-103A-12

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Query Match          100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
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QY      1 EADPTGHSY 9
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Db      1 EADPTGHSY 9

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RESULT 3
US-08-299-849B-26
; Sequence 26, Application US/08299849B
; Patent No. 5612201
; GENERAL INFORMATION:
; APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
; APPLICANT: Leth , Bernard; Szikora, Jean-Pierre; De Smet, Charles;
; APPLICANT: Chomez, Patrick
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
; TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS

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; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,849B
; FILING DATE: 1-SEPTEMBER-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; APPLICATION NUMBER: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-May-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5612201man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5355
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-299-849B-26

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Query Match          100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

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#### RESULT 4

US-08-186-266-1

; Sequence 1, Application US/08186266

; Patent No. 5662907

; GENERAL INFORMATION:

; APPLICANT: KUBO, Ralph T.

; APPLICANT: GREY, Howard M.

; APPLICANT: SETTE, Alessandro

; APPLICANT: CELIS, Esteban

; TITLE OF INVENTION: INDUCTION OF ANTI-TUMOR CYTOTOXIC

; TITLE OF INVENTION: T LYMPHOCYTES IN HUMANS USING

; TITLE OF INVENTION: SYNTHETIC PEPTIDE EPITOPES

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

```

;   ADDRESSEE:  Townsend and Townsend Kourie and Crew
;   STREET:  Steuart Street Tower, One Market Plaza
;   CITY:  San Francisco
;   STATE:  California
;   COUNTRY:  US
;   ZIP:  94105-1493
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/186,266
;   FILING DATE:  25-JAN-1994
;   CLASSIFICATION:  424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/159,339
;   FILING DATE:  29-NOV-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/103,396
;   FILING DATE:  06-AUG-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/027,746
;   FILING DATE:  05-MAR-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/926,666
;   FILING DATE:  07-AUG-1992
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Bastian, Kevin L.
;   REGISTRATION NUMBER:  34,774
;   REFERENCE/DOCKET NUMBER:  14137-50-4
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (415) 543-9600
;   TELEFAX:  (415) 543-5043
;   INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  9 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-186-266-1

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Db      1 EADPTGHSY 9

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RESULT 5
US-08-443-341-12
; Sequence 12, Application US/08443341
; Patent No. 5695994
; GENERAL INFORMATION:
; APPLICANT:  Boon-Falleur, Thierry
; APPLICANT:  van der Bruggen, Pierre
; APPLICANT:  De Plaen, Etienne
; APPLICANT:  Lurquin, Christophe
; APPLICANT:  Traversari, Catia

```

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; APPLICANT: Gaugler, Beatrice
; APPLICANT: Van den Eynde, Benoit
; TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
; TITLE OF INVENTION: MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
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; SOFTWARE: Wordperfect
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; APPLICATION NUMBER: US/08/443,341
; FILING DATE: 17-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,103
; FILING DATE: 7-JUNE-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,334
; FILING DATE: 31-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5695994man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5293.5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-443-341-12

```

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Query Match          100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 6
US-08-787-547-49
; Sequence 49, Application US/08787547
; Patent No. 5783567
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne

```

```

; APPLICANT: Curley, Joanne M.
; APPLICANT: Langer, Robert S.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,547
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-787-547-49

```

```

Query Match          100.0%;  Score 52;  DB 1;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 5e+05;
Matches      9;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 7
US-08-498-461-4
; Sequence 4, Application US/08498461
; Patent No. 5827073
; GENERAL INFORMATION:
; APPLICANT: Luescher, Immanuel; Anjuere, Fabienne;
; APPLICANT: Layer, Andreas; Romero, Pedro; Cerottini, Jean-Charles
; TITLE OF INVENTION: Photoreactive Peptide Derivatives
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue

```

```

; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/498,461
; FILING DATE: 5-JULY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5827073man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5403
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-498-461-4

```

```

Query Match          100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

RESULT 8

US-08-902-516-21

```

; Sequence 21, Application US/08902516
; Patent No. 5891432
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,516
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 424

```

```

; ATTORNEY/AGENT INFORMATION:
;   NAME:  Campbell, Cathryn A.
;   REGISTRATION NUMBER:  31,815
;   REFERENCE/DOCKET NUMBER:  P-IM 2442
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (619)535-9001
;   TELEFAX:  (619)535-8949
; INFORMATION FOR SEQ ID NO:  21:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  9 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-902-516-21

```

```

Query Match          100.0%;  Score 52;  DB 1;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 5e+05;
Matches      9;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 9
US-08-142-368A-26
; Sequence 26, Application US/08142368A
; Patent No. 5925729
; GENERAL INFORMATION:
;   APPLICANT:  Boon-Falleur, Thierry; Van der Bruggen, Thierry;
;   APPLICANT:  Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
;   APPLICANT:  Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
;   TITLE OF INVENTION:  Tumor Rejection Antigen Precursors, Tumor
;   TITLE OF INVENTION:  Rejection Antigens and Uses Thereof
;   NUMBER OF SEQUENCES:  26
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Felfe & Lynch
;     STREET:  805 Third Avenue
;     CITY:  New York City
;     STATE:  New York
;     ZIP:  10022
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;     COMPUTER:  IBM
;     OPERATING SYSTEM:  PC-DOS
;     SOFTWARE:  Wordperfect
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/142,368A
;     FILING DATE:  02-MAY-1994
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/US92/04354
;     FILING DATE:  22-MAY-1992
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  07/807,043
;     FILING DATE:  12-DECEMBER-1991
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  07/764,364
;     FILING DATE:  23-SEPTEMBER-1991
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  07/728,838

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; APPLICATION NUMBER: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-May-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5925729man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5253.4-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-142-368A-26

```

```

Query Match          100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 10
US-09-036-582-1
; Sequence 1, Application US/09036582A
; Patent No. 5965381
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Cornelis, Guy R.
; TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS
; TITLE OF INVENTION: WITH RECOMBINANT YERSINIA
; FILE REFERENCE: 11154
; CURRENT APPLICATION NUMBER: US/09/036,582A
; CURRENT FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human MAGE-1 peptide
US-09-036-582-1

```

```

Query Match          100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 11
US-08-986-234-1
; Sequence 1, Application US/08986234
; Patent No. 5981706

```

```
; GENERAL INFORMATION:
; APPLICANT: Wallen, et al.
; TITLE OF INVENTION: Methods for Synthesizing Heat Shock Protein Complexes
; FILE REFERENCE: UNME-0008-1
; CURRENT APPLICATION NUMBER: US/08/986,234
; CURRENT FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: human
US-08-986-234-1
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```
Query Match          100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
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```
Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9
```

```
RESULT 12
US-08-967-727-26
; Sequence 26, Application US/08967727
; Patent No. 6025474
; GENERAL INFORMATION:
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,727
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,365
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
```



```

; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6025474man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-967-727-26

```

```

Query Match          100.0%; Score 52; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

# RESULT 13

US-08-354-679C-12

```

; Sequence 12, Application US/08354679C
; Patent No. 6034214
; GENERAL INFORMATION:
; APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
; APPLICANT: De Plaen, Etienne; Lurquin Christophe; Traversari, Catia
; TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
; TITLE OF INVENTION: MAGE GENES AND USES THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/354,679C
; FILING DATE: 13-DECEMBER-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,334
; FILING DATE: 31-AUGUST-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BAER, MADELINE F.
; REGISTRATION NUMBER: 36,437
; REFERENCE/DOCKET NUMBER: LUD 5293.2

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-354-679C-12

```

```

Query Match          100.0%; Score 52; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

RESULT 14

US-08-159-339A-99

```

; Sequence 99, Application US/08159339A
; Patent No. 6037135

```

; GENERAL INFORMATION:

```

; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834

```

; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0

```

; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424

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; PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993

```

; ATTORNEY/AGENT INFORMATION:

```

; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US

```

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200  
 ; TELEFAX: (415) 576-0300  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 99:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-08-159-339A-99

Query Match 100.0%; Score 52; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
 |||||  
 Db 1 EADPTGHSY 9

RESULT 15

US-08-795-733B-1

; Sequence 1, Application US/08795733B  
 ; Patent No. 6087441

; GENERAL INFORMATION:

; APPLICANT: Ayyoub, Maha; Monsarrat, Bernard; Mazarg  
 ; APPLICANT: Honor ; Van Der Eynde, Beno t; Gairin, Jean  
 ; APPLICANT: Edouard  
 ; TITLE OF INVENTION: Structurally Modified Peptides  
 ; TITLE OF INVENTION: Resistant to Peptidase Degradation  
 ; NUMBER OF SEQUENCES: 15  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fulbright & Jaworski L.L.P.  
 ; STREET: 666 Fifth Avenue  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
 ; COMPUTER: IBM PS/2  
 ; OPERATING SYSTEM: PC-DOS  
 ; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/795,733B  
 ; FILING DATE: February 13, 1997  
 ; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 6087441man D. Hanson  
 ; REGISTRATION NUMBER: 30,946  
 ; REFERENCE/DOCKET NUMBER: LUD 5461 - JEL/NDH  
 ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200  
 ; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear

; MOLECULE TYPE: protein  
US-08-795-733B-1

Query Match 100.0%; Score 52; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| | | | | | | |  
Db 1 EADPTGHSY 9

Search completed: August 25, 2006, 01:01:08  
Job time : 53 secs

SCORE 1.3 BuildDate: 12/06/2005
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1	52	100.0	9	2	US-08-344-824-18	Sequence 18, Appl
2	52	100.0	9	3	US-09-812-528-1	Sequence 1, Appli
3	52	100.0	9	3	US-09-847-185-21	Sequence 21, Appl
4	52	100.0	9	3	US-09-077-214-9	Sequence 9, Appli
5	52	100.0	9	3	US-09-923-831-4	Sequence 4, Appli
6	52	100.0	9	3	US-09-888-721-23	Sequence 23, Appl
7	52	100.0	9	3	US-09-766-889A-8	Sequence 8, Appli
8	52	100.0	9	3	US-09-909-460-49	Sequence 49, Appl
9	52	100.0	9	3	US-09-789-649-21	Sequence 21, Appl
10	52	100.0	9	3	US-09-872-836-49	Sequence 49, Appl
11	52	100.0	9	4	US-10-161-097-1	Sequence 1, Appli
12	52	100.0	9	4	US-10-128-711-1	Sequence 1, Appli
13	52	100.0	9	4	US-10-224-286-21	Sequence 21, Appl
14	52	100.0	9	4	US-10-170-832-45	Sequence 45, Appl
15	52	100.0	9	4	US-10-239-313A-2	Sequence 2, Appli
16	52	100.0	9	4	US-10-164-121A-19	Sequence 19, Appl
17	52	100.0	9	4	US-10-164-078A-18	Sequence 18, Appl
18	52	100.0	9	4	US-10-406-317-15	Sequence 15, Appl
19	52	100.0	9	4	US-10-447-161-9	Sequence 9, Appli
20	52	100.0	9	4	US-10-218-095-11	Sequence 11, Appl
21	52	100.0	9	4	US-10-367-580-139	Sequence 139, App
22	52	100.0	9	4	US-10-367-593-139	Sequence 139, App
23	52	100.0	9	4	US-10-367-594-139	Sequence 139, App
24	52	100.0	9	4	US-10-367-654-139	Sequence 139, App
25	52	100.0	9	4	US-10-367-658-139	Sequence 139, App
26	52	100.0	9	4	US-10-367-668-139	Sequence 139, App
27	52	100.0	9	4	US-10-297-168-15	Sequence 15, Appl
28	52	100.0	9	4	US-10-258-144-35	Sequence 35, Appl
29	52	100.0	9	4	US-10-367-674-139	Sequence 139, App
30	52	100.0	9	4	US-10-415-841A-43	Sequence 43, Appl
31	52	100.0	9	4	US-10-777-053-409	Sequence 409, App
32	52	100.0	9	4	US-10-777-053-616	Sequence 616, App
33	52	100.0	9	4	US-10-777-053-626	Sequence 626, App
34	52	100.0	9	4	US-10-777-053-933	Sequence 933, App
35	52	100.0	9	4	US-10-777-053-934	Sequence 934, App
36	52	100.0	9	4	US-10-725-952-1	Sequence 1, Appli
37	52	100.0	9	4	US-10-758-673-21	Sequence 21, Appl
38	52	100.0	9	4	US-10-753-158-1	Sequence 1, Appli
39	52	100.0	9	4	US-10-837-217-409	Sequence 409, App
40	52	100.0	9	4	US-10-837-217-616	Sequence 616, App
41	52	100.0	9	4	US-10-837-217-626	Sequence 626, App
42	52	100.0	9	4	US-10-837-217-933	Sequence 933, App
43	52	100.0	9	4	US-10-837-217-934	Sequence 934, App
44	52	100.0	9	4	US-10-670-472A-10	Sequence 10, Appl
45	52	100.0	9	5	US-10-362-715-13	Sequence 13, Appl

#### ALIGNMENTS

```

RESULT 1
US-08-344-824-18
; Sequence 18, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
;   APPLICANT:  SETTE, Alessandro
;   APPLICANT:  SIDNEY, John
;   TITLE OF INVENTION:  HLA BINDING PEPTIDES AND THEIR USES
;   NUMBER OF SEQUENCES:  399
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Townsend and Townsend Khourie and Crew

```

```

; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-18

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Query Match          100.0%; Score 52; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      1 EADPTGHSY 9
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Db      1 EADPTGHSY 9

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RESULT 2
US-09-812-528-1
; Sequence 1, Application US/09812528
; Patent No. US20010018210A1
; GENERAL INFORMATION:
; APPLICANT: Bachovchin, William
; APPLICANT: Wallner, Barbara
; TITLE OF INVENTION: STIMULATION OF HEMATOPOIETIC CELLS IN
; TITLE OF INVENTION: VITRO
; FILE REFERENCE: I0248/7015
; CURRENT APPLICATION NUMBER: US/09/812,528
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/060,306
; PRIOR FILING DATE: 1997-09-29
; PRIOR APPLICATION NUMBER: US 09/162,934
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 3.0

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; SEQ ID NO 1  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-812-528-1

Query Match 100.0%; Score 52; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
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Db 1 EADPTGHSY 9

RESULT 3

US-09-847-185-21

; Sequence 21, Application US/09847185

; Patent No. US20020076392A1

; GENERAL INFORMATION:

; APPLICANT: Soo Hoo, William

; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS

; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
; RESPONSE USING SAME

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CAMPBELL & FLORES, LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/847,185

; FILING DATE: 01-May-2001

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/201,931

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-IM 2442

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619)535-9001

; TELEFAX: (619)535-8949

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-09-847-185-21

Query Match 100.0%; Score 52; DB 3; Length 9;



Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
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Db 1 EADPTGHSY 9

RESULT 4

US-09-077-214-9

; Sequence 9, Application US/09077214  
; Publication No. US20020085997A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Walter  
; APPLICANT: Birnstiel, Max  
; APPLICANT: Schweighoffer, Tamas  
; APPLICANT: Steinlein, Peter  
; APPLICANT: Buschle, Michael  
; TITLE OF INVENTION: Tumor Vaccine And Process For the  
; TITLE OF INVENTION: Preparation Thereof  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/077,214  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 195 43 649.0  
; FILING DATE: 23-NOV-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 196 07 044.9  
; FILING DATE: 24-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fleshner, Raz E.  
; REGISTRATION NUMBER: 34,331  
; REFERENCE/DOCKET NUMBER: 0652.1710000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
US-09-077-214-9

Query Match 100.0%; Score 52; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
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Db 1 EADPTGHSY 9

RESULT 5

US-09-923-831-4

; Sequence 4, Application US/09923831  
; Patent No. US20020115142A1  
; GENERAL INFORMATION:  
; APPLICANT: Martelange, Val,rie  
; APPLICANT: De Smet, Charles  
; APPLICANT: Boon-Falleur, Thierry  
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: L0461/7054  
; CURRENT APPLICATION NUMBER: US/09/923,831  
; CURRENT FILING DATE: 2001-08-07  
; PRIOR APPLICATION NUMBER: 09/183,706  
; PRIOR FILING DATE: 2001-10-30  
; NUMBER OF SEQ ID NOS: 43  
; SEQ ID NO 4  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-923-831-4

Query Match 100.0%; Score 52; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
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Db 1 EADPTGHSY 9

RESULT 6

US-09-888-721-23

; Sequence 23, Application US/09888721  
; Patent No. US20020132990A1  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Wils, Pierre  
; APPLICANT: Zhu, Quan  
; APPLICANT: Laurent, Olivier  
; APPLICANT: Marasco, Wayne A.  
; APPLICANT: Scherman, Daniel  
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID  
; TITLE OF INVENTION: DELIVERY  
; FILE REFERENCE: 23611-A USA  
; CURRENT APPLICATION NUMBER: US/09/888,721  
; CURRENT FILING DATE: 2001-06-25  
; PRIOR APPLICATION NUMBER: 60/213,653  
; PRIOR FILING DATE: 2000-06-23  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-888-721-23

Query Match 100.0%; Score 52; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
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Db 1 EADPTGHSY 9

RESULT 7

US-09-766-889A-8

; Sequence 8, Application US/09766889A  
; Patent No. US20020164654A1  
; GENERAL INFORMATION:  
; APPLICANT: Luiten, Rosalie  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Demotte, Nathalie  
; APPLICANT: Schultz, Erwin  
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44  
; FILE REFERENCE: L0461/7104  
; CURRENT APPLICATION NUMBER: US/09/766,889A  
; CURRENT FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: US 60/177,242  
; PRIOR FILING DATE: 2000-01-20  
; PRIOR APPLICATION NUMBER: US 60/243,212  
; PRIOR FILING DATE: 2000-10-25  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-766-889A-8

Query Match 100.0%; Score 52; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
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Db 1 EADPTGHSY 9

RESULT 8

US-09-909-460-49

; Sequence 49, Application US/09909460  
; Publication No. US20020182258A1  
; GENERAL INFORMATION:  
; APPLICANT: Lunsford, Lynn B.  
; APPLICANT: Putnam, David  
; APPLICANT: Hedley, Mary Lynn  
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC  
; TITLE OF INVENTION: ACID  
; FILE REFERENCE: 08191/014001  
; CURRENT APPLICATION NUMBER: US/09/909,460  
; CURRENT FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 49  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-909-460-49

Query Match 100.0%; Score 52; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
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Db 1 EADPTGHSY 9

RESULT 9

US-09-789-649-21  
; Sequence 21, Application US/09789649  
; Publication No. US20030082804A1  
; GENERAL INFORMATION:  
; APPLICANT: Valmori, Danila  
; APPLICANT: Cerottini, Jean-Charles  
; APPLICANT: Romero, Pedro  
; TITLE OF INVENTION: Isolated No. US20030082804A1a - And Decapeptides Which Bind  
; TITLE OF INVENTION: To HLA Molecules, and the Use Thereof  
; FILE REFERENCE: LUD 5483.2  
; CURRENT APPLICATION NUMBER: US/09/789,649  
; CURRENT FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: US09/099,543  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: US 09/061,388  
; PRIOR FILING DATE: 1998-04-16  
; PRIOR APPLICATION NUMBER: US 08/880,963  
; PRIOR FILING DATE: 1997-06-23  
; NUMBER OF SEQ ID NOS: 32  
; SEQ ID NO 21  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide from MAGE-1 Protein  
US-09-789-649-21

Query Match 100.0%; Score 52; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
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Db 1 EADPTGHSY 9

RESULT 10

US-09-872-836-49  
; Sequence 49, Application US/09872836  
; Publication No. US20040142475A1  
; GENERAL INFORMATION:  
; APPLICANT: Barman, Shikha P.

; APPLICANT: McKeever, Una  
; APPLICANT: Hedley, Mary Lynne  
; TITLE OF INVENTION: DELIVERY SYSTEMS FOR BIOACTIVE AGENTS  
; FILE REFERENCE: 08191-018001  
; CURRENT APPLICATION NUMBER: US/09/872,836  
; CURRENT FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: US 60/208,830  
; PRIOR FILING DATE: 2000-06-02  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 49  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-872-836-49

Query Match 100.0%; Score 52; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| | | | | | | |  
Db 1 EADPTGHSY 9

RESULT 11  
US-10-161-097-1  
; Sequence 1, Application US/10161097  
; Publication No. US20030096404A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSENZWEIG, Michael  
; APPLICANT: PYKETT, Mark J.  
; APPLICANT: SCADDEN, David T.  
; APPLICANT: POZNANSKY, Mark C.  
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION  
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL  
; TITLE OF INVENTION: DEVICES  
; FILE REFERENCE: C1005/7012/KA/ERG  
; CURRENT APPLICATION NUMBER: US/10/161,097  
; CURRENT FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: US/09/574,749  
; PRIOR FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: US 60/107,972  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: PCT/US99/26795  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 09/524,749  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Homo Sapiens source  
US-10-161-097-1

Query Match 100.0%; Score 52; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
|||||||  
Db 1 EADPTGHSY 9

RESULT 12  
US-10-128-711-1  
; Sequence 1, Application US/10128711  
; Publication No. US20030099634A1  
; GENERAL INFORMATION:  
; APPLICANT: VITIELLO, Maria A.  
; CHESTNUT, Robert W.  
; SETTE, Alessandro D.  
; CELIS, Esteban  
; GRAY, Howard  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
; CTL IMMUNITY  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/128,711  
; FILING DATE: 22-Apr-2002  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/197,484  
; FILING DATE: 16-FEB-1994  
; APPLICATION NUMBER: US 07/935,811  
; FILING DATE: 26-AUG-1992  
; APPLICATION NUMBER: US 07/874,491  
; FILING DATE: 27-APR-1992  
; APPLICATION NUMBER: US 07/827,682  
; FILING DATE: 29-JAN-1992  
; APPLICATION NUMBER: US 07/749,568  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parmelee, Steven W.  
; REGISTRATION NUMBER: 31,990  
; REFERENCE/DOCKET NUMBER: 14137-26-4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 467-9600  
; TELEFAX: (206) 623-6793  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-128-711-1

Query Match 100.0%; Score 52; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
|||||||  
Db 1 EADPTGHSY 9

RESULT 13

US-10-224-286-21

; Sequence 21, Application US/10224286

; Publication No. US20030108517A1

; GENERAL INFORMATION:

; APPLICANT: Soo Hoo, William

; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS

; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
; RESPONSE USING SAME

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CAMPBELL & FLORES, LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/224,286

; FILING DATE: 19-Aug-2002

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/902,516

; FILING DATE: 29-JUL-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-IM 2442

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619)535-9001

; TELEFAX: (619)535-8949

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-10-224-286-21

Query Match 100.0%; Score 52; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9

|||||||  
Db 1 EADPTGHSY 9

RESULT 14

US-10-170-832-45

; Sequence 45, Application US/10170832  
; Publication No. US20030170792A1  
; GENERAL INFORMATION:  
; APPLICANT: Chaux, Pascal  
; APPLICANT: Vantomme, Valrie  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Thielemans, Kris  
; APPLICANT: Corthals, Jurgen  
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
; FILE REFERENCE: L0461/7052  
; CURRENT APPLICATION NUMBER: US/10/170,832  
; CURRENT FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: US/09/166,448  
; PRIOR FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 45  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-170-832-45

Query Match 100.0%; Score 52; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
|||||||  
Db 1 EADPTGHSY 9

RESULT 15

US-10-239-313A-2

; Sequence 2, Application US/10239313A  
; Publication No. US20030175285A1  
; GENERAL INFORMATION:  
; APPLICANT: KLINGUER - HAMOUR, Christine  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: BECK, Alain  
; APPLICANT: GOETSCH, Liliane  
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
; FILE REFERENCE: 343 727 - US  
; CURRENT APPLICATION NUMBER: US/10/239,313A  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: FR 00/03711  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: PCT 01/70772  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2



; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-239-313A-2

Query Match 100.0%; Score 52; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
|||||||  
Db 1 EADPTGHSY 9

Search completed: August 25, 2006, 01:15:15  
Job time : 186 secs

SCORE 1.3 BuildDate: 12/06/2005
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# SCORE Search Results Details for Application 08819669 and Search Result us-08-819-669e-26.rapbn.

<a href="#">Score Home Page</a>	<a href="#">Retrieve Application List</a>	<a href="#">SCORE System Overview</a>	<a href="#">SCORE FAQ</a>	<a href="#">Comments / Suggestions</a>
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This page gives you Search Results detail for the Application 08819669 and Search Result us-08-819-669e-26.rapbn.

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OM protein - protein search, using sw model

Run on: August 25, 2006, 01:12:19 ; Search time 32 Seconds  
(without alignments)  
19.244 Million cell updates/sec

Title: US-08-819-669E-26  
Perfect score: 52  
Sequence: 1 EADPTGHSY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	% Query
--------	------------

No.	Score	Match	Length	DB	ID	Description
1	52	100.0	9	6	US-10-497-088-4	Sequence 4, Appli
2	52	100.0	9	7	US-11-253-240-26	Sequence 26, Appl
3	52	100.0	9	7	US-11-313-152-354	Sequence 354, App
4	52	100.0	9	7	US-11-313-152-553	Sequence 553, App
5	52	100.0	9	7	US-11-313-152-563	Sequence 563, App
6	52	100.0	309	7	US-11-323-049-5	Sequence 5, Appli
7	52	100.0	309	7	US-11-323-964-5	Sequence 5, Appli
8	52	100.0	1052	6	US-10-497-088-21	Sequence 21, Appl
9	52	100.0	1342	6	US-10-497-088-14	Sequence 14, Appl
10	42	80.8	9	7	US-11-313-152-558	Sequence 558, App
11	40	76.9	9	7	US-11-313-152-559	Sequence 559, App
12	37	71.2	1049	6	US-10-539-228-343	Sequence 343, App
13	36	69.2	9	6	US-10-538-066-230	Sequence 230, App
14	36	69.2	9	6	US-10-538-066-231	Sequence 231, App
15	36	69.2	9	6	US-10-506-334-2	Sequence 2, Appli
16	36	69.2	9	6	US-10-506-334-19	Sequence 19, Appl
17	36	69.2	9	7	US-11-313-152-357	Sequence 357, App
18	36	69.2	9	7	US-11-313-152-534	Sequence 534, App
19	36	69.2	9	7	US-11-313-152-535	Sequence 535, App
20	36	69.2	9	7	US-11-313-152-551	Sequence 551, App
21	36	69.2	10	6	US-10-538-066-732	Sequence 732, App
22	36	69.2	11	6	US-10-538-066-229	Sequence 229, App
23	36	69.2	11	6	US-10-538-066-723	Sequence 723, App
24	36	69.2	314	6	US-10-538-066-366	Sequence 366, App
25	36	69.2	314	7	US-11-323-049-6	Sequence 6, Appli
26	36	69.2	314	7	US-11-323-964-6	Sequence 6, Appli
27	36	69.2	518	6	US-10-449-902-48443	Sequence 48443, A
28	35	67.3	293	6	US-10-449-902-53971	Sequence 53971, A
29	35	67.3	302	7	US-11-056-355B-83479	Sequence 83479, A
30	35	67.3	526	7	US-11-056-355B-83478	Sequence 83478, A
31	35	67.3	574	7	US-11-056-355B-83477	Sequence 83477, A
32	35	67.3	1139	6	US-10-449-902-52733	Sequence 52733, A
33	35	67.3	1469	7	US-11-330-403-6435	Sequence 6435, Ap
34	34	65.4	299	7	US-11-293-697-3999	Sequence 3999, Ap
35	34	65.4	393	7	US-11-330-403-827	Sequence 827, App
36	33	63.5	9	7	US-11-313-152-557	Sequence 557, App
37	33	63.5	61	6	US-10-449-902-34383	Sequence 34383, A
38	33	63.5	138	6	US-10-953-349-6081	Sequence 6081, Ap
39	33	63.5	138	7	US-11-056-355B-28382	Sequence 28382, A
40	33	63.5	138	7	US-11-056-355B-30643	Sequence 30643, A
41	33	63.5	138	7	US-11-056-355B-31972	Sequence 31972, A
42	33	63.5	138	7	US-11-056-355B-34233	Sequence 34233, A
43	33	63.5	138	7	US-11-056-355B-97528	Sequence 97528, A
44	33	63.5	138	7	US-11-056-355B-102911	Sequence 102911,
45	33	63.5	138	7	US-11-056-355B-108767	Sequence 108767,

#### ALIGNMENTS

##### RESULT 1

US-10-497-088-4

; Sequence 4, Application US/10497088

; Publication No. US20060088520A1

; GENERAL INFORMATION:

; APPLICANT: Crucell Holland B.V.

; APPLICANT: Germeraad, Wilfred

; APPLICANT: Logtenberg, Ton

; APPLICANT: Lekkerkerker, Annemarie N

```

; TITLE OF INVENTION: Antigen presenting cell targeting conjugate, an antigen
; TITLE OF INVENTION: presenting cell contacted with such conjugate, their use for
; TITLE OF INVENTION: vaccination or as medicament, and methods for their production
; TITLE OF INVENTION: generation
; FILE REFERENCE: 0070 US 00 CON
; CURRENT APPLICATION NUMBER: US/10/497,088
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: PCT/EP01/14255
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: PCT/EP02/13681
; PRIOR FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: EP01204997.9
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MAGE-1.A1 specific peptide
US-10-497-088-4

```

```

Query Match          100.0%; Score 52; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 2
US-11-253-240-26
; Sequence 26, Application US/11253240
; Publication No. US20060127356A1
; GENERAL INFORMATION:
; APPLICANT: Gaugler, Batrice; Van den Eynde, BenoEt;
; van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/253,240
; FILING DATE: 17-Oct-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/579,543
; FILING DATE: 26-May-2000
; APPLICATION NUMBER: 09/583,850

```

```

;      FILING DATE:
;      APPLICATION NUMBER: PCT/US92/04354
;      FILING DATE: 22-MAY-1992
;      APPLICATION NUMBER: 07/807,043
;      FILING DATE: 12-DECEMBER-1991
;      APPLICATION NUMBER: 07/764,365
;      FILING DATE: 23-SEPTEMBER-1991
;      APPLICATION NUMBER: 07/728,838
;      FILING DATE: 9-JULY-1991
;      APPLICATION NUMBER: 07/705,702
;      FILING DATE: 23-MAY-1991
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Hanson, Norman D.
;      REGISTRATION NUMBER: 30,946
;      REFERENCE/DOCKET NUMBER: LUD 5353
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (212) 688-9200
;      TELEFAX: (212) 838-3884
;      INFORMATION FOR SEQ ID NO: 26:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 9 amino acids
;      TYPE: amino acids
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-11-253-240-26

```

```

Query Match          100.0%;  Score 52;  DB 7;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 2.3e+05;
Matches      9;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 3
US-11-313-152-354
; Sequence 354, Application US/11313152
; Publication No. US20060153858A1
; GENERAL INFORMATION:
; APPLICANT: Kundig, Thomas M.
; APPLICANT: Simard, John J. L.
; TITLE OF INVENTION: METHOD OF INDUCING A CTL RESPONSE
; FILE REFERENCE: MANNK.001CP2C1
; CURRENT APPLICATION NUMBER: US/11/313,152
; CURRENT FILING DATE: 2005-12-19
; PRIOR APPLICATION NUMBER: 09/776,232
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/380,534
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US98/14289
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 08/988,320
; PRIOR FILING DATE: 1997-12-10
; PRIOR APPLICATION NUMBER: CA 2,209,815
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 569
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 354
; LENGTH: 9

```

; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-11-313-152-354

Query Match 100.0%; Score 52; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| | | | | | | |  
Db 1 EADPTGHSY 9

RESULT 4

US-11-313-152-553  
; Sequence 553, Application US/11313152  
; Publication No. US20060153858A1  
; GENERAL INFORMATION:  
; APPLICANT: Kundig, Thomas M.  
; APPLICANT: Simard, John J. L.  
; TITLE OF INVENTION: METHOD OF INDUCING A CTL RESPONSE  
; FILE REFERENCE: MANNK.001CP2C1  
; CURRENT APPLICATION NUMBER: US/11/313,152  
; CURRENT FILING DATE: 2005-12-19  
; PRIOR APPLICATION NUMBER: 09/776,232  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/380,534  
; PRIOR FILING DATE: 1999-09-01  
; PRIOR APPLICATION NUMBER: PCT/US98/14289  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: 08/988,320  
; PRIOR FILING DATE: 1997-12-10  
; PRIOR APPLICATION NUMBER: CA 2,209,815  
; PRIOR FILING DATE: 1997-07-10  
; NUMBER OF SEQ ID NOS: 569  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 553  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-11-313-152-553

Query Match 100.0%; Score 52; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| | | | | | | |  
Db 1 EADPTGHSY 9

RESULT 5

US-11-313-152-563  
; Sequence 563, Application US/11313152  
; Publication No. US20060153858A1  
; GENERAL INFORMATION:  
; APPLICANT: Kundig, Thomas M.  
; APPLICANT: Simard, John J. L.  
; TITLE OF INVENTION: METHOD OF INDUCING A CTL RESPONSE  
; FILE REFERENCE: MANNK.001CP2C1  
; CURRENT APPLICATION NUMBER: US/11/313,152

```

; CURRENT FILING DATE: 2005-12-19
; PRIOR APPLICATION NUMBER: 09/776,232
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/380,534
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US98/14289
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 08/988,320
; PRIOR FILING DATE: 1997-12-10
; PRIOR APPLICATION NUMBER: CA 2,209,815
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 569
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 563
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-313-152-563

```

```

Query Match          100.0%; Score 52; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

#### RESULT 6

```

US-11-323-049-5
; Sequence 5, Application US/11323049
; Publication No. US20060159694A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; APPLICANT: Diamond, David C.
; APPLICANT: Bot, Adrian Ion
; APPLICANT: Liu, Xiping
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN COMPOSITIONS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.049A
; CURRENT APPLICATION NUMBER: US/11/323,049
; CURRENT FILING DATE: 2005-12-29
; PRIOR APPLICATION NUMBER: 60/640,598
; PRIOR FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-323-049-5

```

```

Query Match          100.0%; Score 52; DB 7; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db     161 EADPTGHSY 169

```

RESULT 7

US-11-323-964-5

```
; Sequence 5, Application US/11323964
; Publication No. US20060159689A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; APPLICANT: Diamond, David C.
; APPLICANT: Bot, Adrian Ion
; APPLICANT: Liu, Xiping
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.050CP1
; CURRENT APPLICATION NUMBER: US/11/323,964
; CURRENT FILING DATE: 2005-12-29
; PRIOR APPLICATION NUMBER: 11/155,288
; PRIOR FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: PCT/US2005/021836
; PRIOR FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-323-964-5
```

```
Query Match          100.0%; Score 52; DB 7; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      1 EADPTGHSY 9
        |||||
Db      161 EADPTGHSY 169
```

RESULT 8

US-10-497-088-21

```
; Sequence 21, Application US/10497088
; Publication No. US20060088520A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Germeraad, Wilfred
; APPLICANT: Logtenberg, Ton
; APPLICANT: Lekkerkerker, Annemarie N
; TITLE OF INVENTION: Antigen presenting cell targeting conjugate, an antigen
; TITLE OF INVENTION: presenting cell contacted with such conjugate, their use for
; TITLE OF INVENTION: vaccination or as medicament, and methods for their production
; TITLE OF INVENTION: generation
; FILE REFERENCE: 0070 US 00 CON
; CURRENT APPLICATION NUMBER: US/10/497,088
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: PCT/EP01/14255
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: PCT/EP02/13681
; PRIOR FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: EP01204997.9
; PRIOR FILING DATE: 2001-12-19
```



```
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
;   LENGTH: 1052
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: MatDC16-Cgamma4-MAGE-1
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (546)..(546)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-497-088-21
```

```
Query Match          100.0%;  Score 52;  DB 6;  Length 1052;
Best Local Similarity 100.0%;  Pred. No. 0.11;
Matches      9;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;
```

```
Qy      1 EADPTGHSY 9
        |||||
Db      904 EADPTGHSY 912
```

RESULT 9

US-10-497-088-14

```
; Sequence 14, Application US/10497088
; Publication No. US20060088520A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Germeraad, Wilfred
; APPLICANT: Logtenberg, Ton
; APPLICANT: Lekkerkerker, Annemarie N
; TITLE OF INVENTION: Antigen presenting cell targeting conjugate, an antigen
; TITLE OF INVENTION: presenting cell contacted with such conjugate, their use for
; TITLE OF INVENTION: vaccination or as medicament, and methods for their production
; TITLE OF INVENTION: generation
; FILE REFERENCE: 0070 US 00 CON
; CURRENT APPLICATION NUMBER: US/10/497,088
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: PCT/EP01/14255
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: PCT/EP02/13681
; PRIOR FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: EP01204997.9
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
;   LENGTH: 1342
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: MatDC16-Cgamma4-MAGE-A1
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (836)..(836)
;   OTHER INFORMATION: Xaa can be any amino acid
US-10-497-088-14
```

```
Query Match          100.0%;  Score 52;  DB 6;  Length 1342;
Best Local Similarity 100.0%;  Pred. No. 0.14;
```

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
|||||||  
Db 161 EADPTGHSY 169

RESULT 10

US-11-313-152-558

; Sequence 558, Application US/11313152  
; Publication No. US20060153858A1  
; GENERAL INFORMATION:  
; APPLICANT: Kundig, Thomas M.  
; APPLICANT: Simard, John J. L.  
; TITLE OF INVENTION: METHOD OF INDUCING A CTL RESPONSE  
; FILE REFERENCE: MANNK.001CP2C1  
; CURRENT APPLICATION NUMBER: US/11/313,152  
; CURRENT FILING DATE: 2005-12-19  
; PRIOR APPLICATION NUMBER: 09/776,232  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/380,534  
; PRIOR FILING DATE: 1999-09-01  
; PRIOR APPLICATION NUMBER: PCT/US98/14289  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: 08/988,320  
; PRIOR FILING DATE: 1997-12-10  
; PRIOR APPLICATION NUMBER: CA 2,209,815  
; PRIOR FILING DATE: 1997-07-10  
; NUMBER OF SEQ ID NOS: 569  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 558  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(9)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-11-313-152-558

Query Match 80.8%; Score 42; DB 7; Length 9;  
Best Local Similarity 77.8%; Pred. No. 2.3e+05;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
|||| |||  
Db 1 EADPIGHXY 9

RESULT 11

US-11-313-152-559

; Sequence 559, Application US/11313152  
; Publication No. US20060153858A1  
; GENERAL INFORMATION:  
; APPLICANT: Kundig, Thomas M.  
; APPLICANT: Simard, John J. L.  
; TITLE OF INVENTION: METHOD OF INDUCING A CTL RESPONSE  
; FILE REFERENCE: MANNK.001CP2C1  
; CURRENT APPLICATION NUMBER: US/11/313,152  
; CURRENT FILING DATE: 2005-12-19  
; PRIOR APPLICATION NUMBER: 09/776,232

```

; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/380,534
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US98/14289
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 08/988,320
; PRIOR FILING DATE: 1997-12-10
; PRIOR APPLICATION NUMBER: CA 2,209,815
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 569
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 559
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-11-313-152-559

```

```

Query Match          76.9%;   Score 40;   DB 7;   Length 9;
Best Local Similarity 77.8%;   Pred. No. 2.3e+05;
Matches      7;   Conservative    0;   Mismatches    2;   Indels      0;   Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||| || |
Db      1 EADPIGHLY 9

```

#### RESULT 12

```

US-10-539-228-343
; Sequence 343, Application US/10539228
; Publication No. US20060154250A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: CHIR0052-101 (PP023370.0003)
; CURRENT APPLICATION NUMBER: US/10/539,228
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 343
;   LENGTH: 1049
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-539-228-343

```

```

Query Match          71.2%;   Score 37;   DB 6;   Length 1049;
Best Local Similarity 100.0%;   Pred. No. 68;
Matches      6;   Conservative    0;   Mismatches    0;   Indels      0;   Gaps      0;

```

```

Qy      4 PTGHSY 9
        |||||
Db      52 PTGHSY 57

```

#### RESULT 13

```

US-10-538-066-230
; Sequence 230, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; TITLE OF INVENTION: Peptides and Compositions
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 230
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-230

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Query Match          69.2%; Score 36; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.3e+05;
Matches      6; Conservative      0; Mismatches      3; Indels      0; Gaps      0;

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Qy      1 EADPTGHSY 9
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Db      1 EVDPIGHLy 9

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#### RESULT 14

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US-10-538-066-231
; Sequence 231, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; TITLE OF INVENTION: Peptides and Compositions
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 231
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-231

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Query Match          69.2%; Score 36; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.3e+05;
Matches      6; Conservative      0; Mismatches      3; Indels      0; Gaps      0;

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Qy      1 EADPTGHSY 9
        | || || |
Db      1 ETDPIGHLy 9

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#### RESULT 15

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US-10-506-334-2
; Sequence 2, Application US/10506334
; Publication No. US20060122119A1
; GENERAL INFORMATION:
; APPLICANT: LINARD, BORIS

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; APPLICANT: JOTEREAU, FRANCINE
; APPLICANT: BENLALAM, HOUSSEM
; APPLICANT: DIEZ, ELIZABETH
; APPLICANT: GUILLOUX, YANNICK
; APPLICANT: LABARRIERE, NATHALIE
; APPLICANT: GERVOIS, NADINE
; APPLICANT: DERRE, LAURENT
; TITLE OF INVENTION: PEPTIDES FOR USE IN ANTITUMOR IMMUNOTHERAPY
; FILE REFERENCE: 258087USOXPCT
; CURRENT APPLICATION NUMBER: US/10/506,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: PCT/FR03/00698
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: FR 02/02703
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-506-334-2

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Query Match          69.2%; Score 36; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.3e+05;
Matches      6; Conservative      0; Mismatches      3; Indels      0; Gaps      0;

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Qy      1 EADPTGHSY 9
        | |||||
Db      1 EVDPIGHVY 9

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Search completed: August 25, 2006, 01:15:52  
Job time : 33 secs

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SCORE 1.3 BuildDate: 12/06/2005

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# SCORE Search Results Details for Application 08819669 and Search Result us-08-819-669e 26.rapm.

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This page gives you Search Results detail for the Application 08819669 and Search Result us-08-81 26.rapm.

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2006, 01:00:27 ; Search time 604 Seconds  
(without alignments)  
22.753 Million cell updates/sec

Title: US-08-819-669E-26  
Perfect score: 52  
Sequence: 1 EADPTGHSY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 8366291 seqs, 1526956180 residues

Total number of hits satisfying chosen parameters: 8366291

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	52	100.0	9	1	PCT-US00-04326-8	Sequence 8, Appli
3	52	100.0	9	1	PCT-US00-25559-3	Sequence 3, Appli
4	52	100.0	9	1	PCT-US01-20182-23	Sequence 23, Appl
5	52	100.0	9	1	PCT-US03-16736-9	Sequence 9, Appli
6	52	100.0	9	1	PCT-US03-17641-20	Sequence 20, Appl
7	52	100.0	9	1	PCT-US03-30031A-10	Sequence 10, Appl
8	52	100.0	9	1	PCT-US04-04340-118	Sequence 118, App
9	52	100.0	9	1	PCT-US05-10597-1	Sequence 1, Appli
10	52	100.0	9	1	PCT-US98-01499-49	Sequence 49, Appl
11	52	100.0	9	1	PCT-US99-20344-16	Sequence 16, Appl
12	52	100.0	9	9	US-07-926-666-27	Sequence 27, Appl
13	52	100.0	9	10	US-08-027-746-49	Sequence 49, Appl
14	52	100.0	9	11	US-08-103-396A-54	Sequence 54, Appl
15	52	100.0	9	11	US-08-103-396A-549	Sequence 549, App
16	52	100.0	9	11	US-08-103-396A-634	Sequence 634, App

17	52	100.0	9	11	US-08-103-396A-657	Sequence 657, App
18	52	100.0	9	12	US-08-233-496A-2	Sequence 2, Appli
19	52	100.0	9	12	US-08-261-541A-1	Sequence 1, Appli
20	52	100.0	9	12	US-08-278-634-13	Sequence 13, Appl
21	52	100.0	9	13	US-08-315-961A-26	Sequence 26, Appl
22	52	100.0	9	13	US-08-344-824-18	Sequence 18, Appl
23	52	100.0	9	13	US-08-344-824A-18	Sequence 18, Appl
24	52	100.0	9	13	US-08-347-610-356	Sequence 356, App
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29	52	100.0	9	13	US-08-354-679B-12	Sequence 12, Appl
30	52	100.0	9	16	US-08-651-925-67	Sequence 67, Appl
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34	52	100.0	9	18	US-08-819-669D-26	Sequence 26, Appl
35	52	100.0	9	18	US-08-819-669E-26	Sequence 26, Appl
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37	52	100.0	9	18	US-08-880-979-3	Sequence 3, Appli
38	52	100.0	9	19	US-08-922-869-12	Sequence 12, Appl
39	52	100.0	9	19	US-08-922-869A-12	Sequence 12, Appl
40	52	100.0	9	19	US-08-922-869B-12	Sequence 12, Appl
41	52	100.0	9	19	US-08-944-744-1	Sequence 1, Appli
42	52	100.0	9	19	US-08-992-124-1	Sequence 1, Appli
43	52	100.0	9	20	US-09-003-253-49	Sequence 49, Appl
44	52	100.0	9	20	US-09-049-850-6	Sequence 6, Appli
45	52	100.0	9	20	US-09-060-706-4	Sequence 4, Appli

#### ALIGNMENTS

##### RESULT 1

PCT-IL03-00501A-30

; Sequence 30, Application PC/TIL0300501A

; GENERAL INFORMATION:

; APPLICANT: GAVISH-GALILEE BIO APPLICATIONS LTD.

; APPLICANT: GROSS, Gideon

; APPLICANT: MARGALIT, Alon

; TITLE OF INVENTION: MEMBRANE-ANCHORED BETA-2 MICROGLOBULIN COVALENTLY LINKED TO MHC

; TITLE OF INVENTION: PEPTIDE EPITOPES

; FILE REFERENCE: GAVISH-004 PCT

; CURRENT APPLICATION NUMBER: PCT/IL03/00501A

; CURRENT FILING DATE: 2003-06-12

; PRIOR APPLICATION NUMBER: US 60/388,273

; PRIOR FILING DATE: 2002-06-12

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 30

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

PCT-IL03-00501A-30

Query Match 100.0%; Score 52; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 7.7e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 1 EADPTGHSY 9  
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Db 1 EADPTGHSY 9

RESULT 2

PCT-US00-04326-8

; Sequence 8, Application PC/TUS0004326

; GENERAL INFORMATION:

; APPLICANT: Chiari, Rita

; APPLICANT: Coulie, Pierre G.

; APPLICANT: Boon-Falleur, Thierry

; TITLE OF INVENTION: TYROSINE KINASE RECEPTOR EphA3 ANTIGENIC PEPTIDES

; FILE REFERENCE: L0461/7057WO

; CURRENT APPLICATION NUMBER: PCT/US00/04326

; CURRENT FILING DATE: 2000-02-18

; EARLIER APPLICATION NUMBER: US 60/121,170

; EARLIER FILING DATE: 1999-02-22

; EARLIER APPLICATION NUMBER: US 60/158,566

; EARLIER FILING DATE: 1999-10-08

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 8

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US00-04326-8

Query Match 100.0%; Score 52; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 EADPTGHSY 9

RESULT 3

PCT-US00-25559-3

; Sequence 3, Application PC/TUS0025559

; GENERAL INFORMATION:

; APPLICANT: Zycos Inc.

; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES

; FILE REFERENCE: 08191-013WO1

; CURRENT APPLICATION NUMBER: PCT/US00/25559

; CURRENT FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: PCT/US00/25559

; PRIOR FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: US 60/169,846

; PRIOR FILING DATE: 1999-12-09

; PRIOR APPLICATION NUMBER: US 60/154,665

; PRIOR FILING DATE: 1999-09-16

; NUMBER OF SEQ ID NOS: 163

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US00-25559-3

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Best Local Similarity 100.0%; Pred. No. 7.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
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Db 1 EADPTGHSY 9

RESULT 4

PCT-US01-20182-23  
; Sequence 23, Application PC/TUS0120182  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Wils, Pierre  
; APPLICANT: Zhu, Quan  
; APPLICANT: Laurent, Olivier  
; APPLICANT: Marasco, Wayne A.  
; APPLICANT: Scherman, Daniel  
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID  
; TITLE OF INVENTION: DELIVERY  
; FILE REFERENCE: 23611-A USA  
; CURRENT APPLICATION NUMBER: PCT/US01/20182  
; CURRENT FILING DATE: 2001-06-25  
; PRIOR APPLICATION NUMBER: 60/213,653  
; PRIOR FILING DATE: 2000-06-23  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US01-20182-23

Query Match 100.0%; Score 52; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
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Db 1 EADPTGHSY 9

RESULT 5

PCT-US03-16736-9  
; Sequence 9, Application PC/TUS0316736  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Rong-fu  
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis  
; FILE REFERENCE: HO-P02484W00  
; CURRENT APPLICATION NUMBER: PCT/US03/16736  
; CURRENT FILING DATE: 2003-05-28  
; PRIOR APPLICATION NUMBER: 60/383,530  
; PRIOR FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Synthetic Peptide  
PCT-US03-16736-9

Query Match 100.0%; Score 52; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
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RESULT 6

PCT-US03-17641-20

; Sequence 20, Application PC/TUS0317641

; GENERAL INFORMATION:

; APPLICANT: Bilsborough, Janine

; APPLICANT: Zhang, Yi

; APPLICANT: Schultz, Erwin

; APPLICANT: Panichelli, Christophe

; APPLICANT: Van der Bruggen, Pierre

; APPLICANT: Boon-Falleur, Thierry

; APPLICANT: Traversari, Catia

; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B18 and Cw16 Molecules And

; TITLE OF INVENTION: Thereof

; FILE REFERENCE: LUD-5756.1 PCT

; CURRENT APPLICATION NUMBER: PCT/US03/17641

; CURRENT FILING DATE: 2003-06-04

; PRIOR APPLICATION NUMBER: US 10/164,078

; PRIOR FILING DATE: 2002-06-05

; PRIOR APPLICATION NUMBER: US 10/164,121

; PRIOR FILING DATE: 2002-06/05

; NUMBER OF SEQ ID NOS: 37

; SEQ ID NO 20

; LENGTH: 9

; TYPE: PRT

; ORGANISM: H. sapiens

; FEATURE:

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 EADPTGHSY 9

RESULT 7

PCT-US03-30031A-10

; Sequence 10, Application PC/TUS0330031A

; GENERAL INFORMATION:

; APPLICANT: LUDWIG INSTITUTE FOR CANCER RESEARCH

; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF

; FILE REFERENCE: LUD 5780.2 PCT

; CURRENT APPLICATION NUMBER: PCT/US03/30031A

; CURRENT FILING DATE: 2003-09-26

; PRIOR APPLICATION NUMBER: 60/413,844

; PRIOR FILING DATE: 2002-09-27

; PRIOR APPLICATION NUMBER: 60/433,983

; PRIOR FILING DATE: 2002-12-18  
; PRIOR APPLICATION NUMBER: 60/459,263  
; PRIOR FILING DATE: 2003-04-02  
; NUMBER OF SEQ ID NOS: 105  
; SOFTWARE: PatentIn version 3.3  
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; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US03-30031A-10

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 EADPTGHSY 9

RESULT 8

PCT-US04-04340-118  
; Sequence 118, Application PC/TUS0404340  
; GENERAL INFORMATION:  
; APPLICANT: Antigenics, Inc.  
; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED VACCINES AND  
; TITLE OF INVENTION: IMMUNOTHERAPIES  
; FILE REFERENCE: 8449-405-228  
; CURRENT APPLICATION NUMBER: PCT/US04/04340  
; CURRENT FILING DATE: 2004-02-13  
; PRIOR APPLICATION NUMBER: 60/503,417  
; PRIOR FILING DATE: 2003-09-16  
; PRIOR APPLICATION NUMBER: 60/463,746  
; PRIOR FILING DATE: 2003-04-18  
; PRIOR APPLICATION NUMBER: 60/462,469  
; PRIOR FILING DATE: 2003-04-11  
; PRIOR APPLICATION NUMBER: 60/447,142  
; PRIOR FILING DATE: 2003-02-13  
; NUMBER OF SEQ ID NOS: 419  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 118  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US04-04340-118

Query Match 100.0%; Score 52; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 EADPTGHSY 9

RESULT 9

PCT-US05-10597-1  
; Sequence 1, Application PC/TUS0510597  
; GENERAL INFORMATION:  
; APPLICANT: Cytomatrix, LLC  
; APPLICANT: Pykett, Mark J.

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; APPLICANT:  Rosenzweig, Michael
; TITLE OF INVENTION:  METHODS FOR PRODUCTION OF REGULATORY T CELLS AND USES THEREOF
; FILE REFERENCE:  C1005.70014WO00
; CURRENT APPLICATION NUMBER:  PCT/US05/10597
; CURRENT FILING DATE:  2005-03-29
; PRIOR APPLICATION NUMBER:  US 60/557,669
; PRIOR FILING DATE:  2004-03-29
; NUMBER OF SEQ ID NOS:  58
; SOFTWARE:  PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH:  9
;   TYPE:  PRT
;   ORGANISM:  Artificial sequence
;   FEATURE:
;   OTHER INFORMATION:  Homo sapiens source
PCT-US05-10597-1

```

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Query Match          100.0%;  Score 52;  DB 1;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 7.7e+06;
Matches      9;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 10
PCT-US98-01499-49
; Sequence 49, Application PC/TUS9801499
; GENERAL INFORMATION:
;   APPLICANT:  Pangaea, Inc.
;   TITLE OF INVENTION:  MICROPARTICLES FOR DELIVERY
;   TITLE OF INVENTION:  OF NUCLEIC ACID
;   NUMBER OF SEQUENCES:  107
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Fish & Richardson, P.C.
;     STREET:  225 Franklin Street
;     CITY:  Boston
;     STATE:  MA
;     COUNTRY:  US
;     ZIP:  02110-2804
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Diskette
;     COMPUTER:  IBM Compatible
;     OPERATING SYSTEM:  Windows95
;     SOFTWARE:  FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/US98/01499
;     FILING DATE:  22-JAN-1998
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/787,547
;     FILING DATE:  22-JAN-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Fraser, Janis K.
;     REGISTRATION NUMBER:  34,819
;     REFERENCE/DOCKET NUMBER:  08191/003WO1
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  617-542-5070
;     TELEFAX:  617-542-8906
;     TELEX:  200154
;   INFORMATION FOR SEQ ID NO:  49:

```

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
PCT-US98-01499-49

Query Match 100.0%; Score 52; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
|||||||  
Db 1 EADPTGHSY 9

RESULT 11  
PCT-US99-20344-16  
; Sequence 16, Application PC/TUS9920344  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research  
; TITLE OF INVENTION: AN ANTIGENIC PEPTIDE ENCODED BY AN ALTERNATIVE OPEN READING FRA  
; TITLE OF INVENTION: HUMAN MACROPHAGE COLONY-STIMULATING FACTOR  
; FILE REFERENCE: L0461/7040WO  
; CURRENT APPLICATION NUMBER: PCT/US99/20344  
; CURRENT FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSEQ for Window Version 3.0  
; SEQ ID NO 16  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US99-20344-16

Query Match 100.0%; Score 52; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
|||||||  
Db 1 EADPTGHSY 9

RESULT 12  
US-07-926-666-27  
; Sequence 27, Application US/07926666  
; GENERAL INFORMATION:  
; APPLICANT: KUDO, RALPH T  
; APPLICANT: GREY, HOWARD M  
; APPLICANT: SETTE, ALESSANDRO  
; APPLICANT: CELIS, ESTEBAN  
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND AND TOWNSEND KHOURIE AND CREW  
; STREET: 1 MARKET PLAZA, STEUART TOWER, SUITE 2000  
; CITY: SAN FRANCISCO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/926,666
; FILING DATE: 19920807
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: BASTIAN, KEVIN L
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-50
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-926-666-27

```

```

Query Match          100.0%; Score 52; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 13
US-08-027-746-49
; Sequence 49, Application US/08027746
; GENERAL INFORMATION:
; APPLICANT: KUBO, Ralph T.
; APPLICANT: GREY, Howard M.
; APPLICANT: SETTE, Alessandro
; APPLICANT: CELIS, Esteban
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 249
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/027,746
; FILING DATE: 19930305
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774

```

; REFERENCE/DOCKET NUMBER: 14137-50-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-08-027-746-49

Query Match 100.0%; Score 52; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| | | | | | | |  
Db 1 EADPTGHSY 9

RESULT 14

US-08-103-396A-54

; Sequence 54, Application US/08103396A  
; GENERAL INFORMATION:  
; APPLICANT: KUBO, Ralph T.  
; APPLICANT: GREY, Howard M.  
; APPLICANT: SETTE, Alessandro  
; APPLICANT: CELIS, Esteban  
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES  
; NUMBER OF SEQUENCES: 662  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/103,396A  
; FILING DATE: 06-AUG-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/926,666  
; FILING DATE: 07-JUL-1992  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/027,746  
; FILING DATE: 05-MAR-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 14137-50-2



```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-103-396A-54

```

```

Query Match          100.0%; Score 52; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

# RESULT 15

US-08-103-396A-549

; Sequence 549, Application US/08103396A

## ; GENERAL INFORMATION:

```

; APPLICANT: KUBO, Ralph T.
; APPLICANT: GREY, Howard M.
; APPLICANT: SETTE, Alessandro
; APPLICANT: CELIS, Esteban
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 662
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1492

```

## ; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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## ; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/103,396A
; FILING DATE: 06-AUG-1993
; CLASSIFICATION: 424

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## ; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-JUL-1992
; CLASSIFICATION: 424

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## ; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; CLASSIFICATION: 424

```

## ; ATTORNEY/AGENT INFORMATION:

```

; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-50-2

```

## ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 549:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-103-396A-549

Query Match 100.0%; Score 52; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| | | | | | | |  
Db 1 EADPTGHSY 9

Search completed: August 25, 2006, 01:11:18  
Job time : 605 secs

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SCORE 1.3 BuildDate: 12/06/2005

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# SCORE Search Results Details for Application 08819669 and Search Result us-08-819-669e- 26.rapn.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

This page gives you Search Results detail for the Application 08819669 and Search Result us-08-819-669e-26.rapn.

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OM protein - protein search, using sw model

Run on: August 25, 2006, 01:01:22 ; Search time 40 Seconds  
(without alignments)  
19.416 Million cell updates/sec

Title: US-08-819-669E-26  
Perfect score: 52  
Sequence: 1 EADPTGHSY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 361526 seqs, 86294087 residues

Total number of hits satisfying chosen parameters: 361526

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/1/paa/PCT\_NEW\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/1/paa/US06\_NEW\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/1/paa/US07\_NEW\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/1/paa/US09\_NEW\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/1/paa/US10\_NEW\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/1/paa/US11\_NEW\_COMB.pep:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	% Query
--------	------------

No.	Score	Match	Length	DB	ID	Description
1	52	100.0	9	6	US-10-362-715A-13	Sequence 13, Appl
2	52	100.0	9	6	US-10-497-088A-4	Sequence 4, Appli
3	52	100.0	9	6	US-10-447-161A-9	Sequence 9, Appli
4	52	100.0	9	7	US-11-375-226A-3	Sequence 3, Appli
5	52	100.0	309	6	US-10-657-022A-71	Sequence 71, Appl
6	52	100.0	445	5	US-09-601-565D-7	Sequence 7, Appli
7	52	100.0	446	5	US-09-601-565D-4	Sequence 4, Appli
8	52	100.0	1342	6	US-10-497-088A-14	Sequence 14, Appl
9	44	84.6	369	7	US-11-371-354-73367	Sequence 73367, A
10	43	82.7	315	7	US-11-371-354-69197	Sequence 69197, A
11	43	82.7	318	7	US-11-371-354-71659	Sequence 71659, A
12	42	80.8	319	7	US-11-371-354-73341	Sequence 73341, A
13	37	71.2	1049	6	US-10-669-920-860	Sequence 860, App
14	36	69.2	9	6	US-10-362-715A-12	Sequence 12, Appl
15	36	69.2	10	6	US-10-362-715A-23	Sequence 23, Appl
16	36	69.2	10	6	US-10-447-161A-25	Sequence 25, Appl
17	36	69.2	314	6	US-10-657-022A-73	Sequence 73, Appl
18	36	69.2	314	7	US-11-439-334-2	Sequence 2, Appli
19	36	69.2	314	7	US-11-371-354-69501	Sequence 69501, A
20	36	69.2	372	6	US-10-510-953-38	Sequence 38, Appl
21	36	69.2	389	7	US-11-442-668-23	Sequence 23, Appl
22	36	69.2	403	5	US-09-601-565D-5	Sequence 5, Appli
23	36	69.2	428	6	US-10-553-674-53	Sequence 53, Appl
24	36	69.2	450	5	US-09-601-565D-2	Sequence 2, Appli
25	36	69.2	453	5	US-09-601-565D-9	Sequence 9, Appli
26	36	69.2	599	7	US-11-442-668-59	Sequence 59, Appl
27	35	67.3	346	7	US-11-371-354-12740	Sequence 12740, A
28	35	67.3	346	7	US-11-371-354-65581	Sequence 65581, A
29	35	67.3	346	7	US-11-371-354-76818	Sequence 76818, A
30	35	67.3	359	1	PCT-US06-18535-8064	Sequence 8064, Ap
31	35	67.3	359	7	US-11-431-855-8064	Sequence 8064, Ap
32	35	67.3	561	8	US-60-836-986-30881	Sequence 30881, A
33	35	67.3	734	7	US-11-431-708-2503	Sequence 2503, Ap
34	35	67.3	734	7	US-11-475-062-6125	Sequence 6125, Ap
35	35	67.3	734	8	US-60-812-075-13	Sequence 13, Appl
36	35	67.3	873	7	US-11-431-708-2258	Sequence 2258, Ap
37	35	67.3	873	7	US-11-475-062-3172	Sequence 3172, Ap
38	35	67.3	873	8	US-60-819-940-70	Sequence 70, Appl
39	35	67.3	873	8	US-60-812-075-14	Sequence 14, Appl
40	35	67.3	925	7	US-11-431-708-2259	Sequence 2259, Ap
41	35	67.3	925	7	US-11-475-062-3173	Sequence 3173, Ap
42	35	67.3	925	8	US-60-812-075-15	Sequence 15, Appl
43	35	67.3	931	7	US-11-431-708-2261	Sequence 2261, Ap
44	35	67.3	931	7	US-11-475-062-3175	Sequence 3175, Ap
45	35	67.3	931	8	US-60-812-075-16	Sequence 16, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-362-715A-13

; Sequence 13, Application US/10362715A

; GENERAL INFORMATION:

; APPLICANT: Schuler, Gerold

; APPLICANT: Schuler-Thurner, Beatrice

; TITLE OF INVENTION: METHOD FOR READY-TO-USE, ANTIGEN LOADED OR UNLOADED,

; TITLE OF INVENTION: CRYOCONSERVED MATURE DENDRITIC CELLS

; FILE REFERENCE: ARG015

; CURRENT APPLICATION NUMBER: US/10/362,715A  
; CURRENT FILING DATE: 2003-06-25  
; PRIOR APPLICATION NUMBER: PCT/EP01/09790  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: DE 10041515.6  
; PRIOR FILING DATE: 2000-08-24  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 13  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-362-715A-13

Query Match 100.0%; Score 52; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.2e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| | | | | | | |  
Db 1 EADPTGHSY 9

RESULT 2

US-10-497-088A-4

; Sequence 4, Application US/10497088A  
; GENERAL INFORMATION:  
; APPLICANT: Germeraad, Wilfred  
; APPLICANT: Logtenberg, Ton  
; APPLICANT: Lekkerkerker, Annemarie N  
; TITLE OF INVENTION: Antigen presenting cell targeting conjugate, an antigen  
; TITLE OF INVENTION: presenting cell contacted with such conjugate, their use  
; TITLE OF INVENTION: for vaccination or as medicament, and methods for their  
; TITLE OF INVENTION: production or generation  
; FILE REFERENCE: 0070 US 00 CON  
; CURRENT APPLICATION NUMBER: US/10/497,088A  
; CURRENT FILING DATE: 2005-06-20  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: MAGE-1.A1 specific peptide  
US-10-497-088A-4

Query Match 100.0%; Score 52; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.2e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| | | | | | | |  
Db 1 EADPTGHSY 9

RESULT 3

US-10-447-161A-9

; Sequence 9, Application US/10447161A  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Rong Fu

```

; TITLE OF INVENTION: MUTANT FIBRONECTIN AND TUMOR METASTASIS
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161A
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161A-9

```

```

Query Match          100.0%; Score 52; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 4
US-11-375-226A-3
; Sequence 3, Application US/11375226A
; GENERAL INFORMATION:
; APPLICANT: Yang, Yuh-Cheng
; APPLICANT: Tsao, Yeou-Ping
; APPLICANT: Chen, Show-Li
; TITLE OF INVENTION: A PEPTIDE ANTIGEN OF HUMAN PAPILLOMAVIRUS TYPE 16 AND APPLICATI
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 943371-IE1
; CURRENT APPLICATION NUMBER: US/11/375,226A
; CURRENT FILING DATE: 2006-03-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: melanoma antigen-1 peptide 161-169(negative control)
US-11-375-226A-3

```

```

Query Match          100.0%; Score 52; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 5
US-10-657-022A-71
; Sequence 71, Application US/10657022A
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.

```

```
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPI TOPE SEQUENCES
; FILE REFERENCE: MANNK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022A
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: 60/409,123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 690
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-657-022A-71
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```
Query Match          100.0%;  Score 52;  DB 6;  Length 309;
Best Local Similarity 100.0%;  Pred. No. 0.035;
Matches      9;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;
```

```
Qy      1 EADPTGHSY 9
        |||||
Db      161 EADPTGHSY 169
```

#### RESULT 6

```
US-09-601-565D-7
; Sequence 7, Application US/09601565D
; GENERAL INFORMATION:
; APPLICANT: Smith Kline Beecham Biologicals
; TITLE OF INVENTION: Processes for the Production of Therapeutic Compositions
; FILE REFERENCE: B45126
; CURRENT APPLICATION NUMBER: US/09/601,565D
; CURRENT FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein of CLYTA-MAGE1-Histidine
US-09-601-565D-7
```

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Query Match          100.0%;  Score 52;  DB 5;  Length 445;
Best Local Similarity 100.0%;  Pred. No. 0.052;
Matches      9;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;
```

```
Qy      1 EADPTGHSY 9
        |||||
Db      288 EADPTGHSY 296
```

#### RESULT 7

```
US-09-601-565D-4
; Sequence 4, Application US/09601565D
; GENERAL INFORMATION:
; APPLICANT: Smith Kline Beecham Biologicals
; TITLE OF INVENTION: Processes for the Production of Therapeutic Compositions
; FILE REFERENCE: B45126
```

; CURRENT APPLICATION NUMBER: US/09/601,565D  
; CURRENT FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4  
; LENGTH: 446  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Fusion protein of LPD-MAGE1-Histidine  
US-09-601-565D-4

Query Match 100.0%; Score 52; DB 5; Length 446;  
Best Local Similarity 100.0%; Pred. No. 0.052;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| | | | | | | |  
Db 289 EADPTGHSY 297

RESULT 8

US-10-497-088A-14  
; Sequence 14, Application US/10497088A  
; GENERAL INFORMATION:  
; APPLICANT: Germeraad, Wilfred  
; APPLICANT: Logtenberg, Ton  
; APPLICANT: Lekkerkerker, Annemarie N  
; TITLE OF INVENTION: Antigen presenting cell targeting conjugate, an antigen  
; TITLE OF INVENTION: presenting cell contacted with such conjugate, their use  
; TITLE OF INVENTION: for vaccination or as medicament, and methods for their  
; TITLE OF INVENTION: production or generation  
; FILE REFERENCE: 0070 US 00 CON  
; CURRENT APPLICATION NUMBER: US/10/497,088A  
; CURRENT FILING DATE: 2005-06-20  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 14  
; LENGTH: 1342  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: MatDC16-Cgamma4-MAGE-A1  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (836)..(836)  
; OTHER INFORMATION: Unsure amino acid  
US-10-497-088A-14

Query Match 100.0%; Score 52; DB 6; Length 1342;  
Best Local Similarity 100.0%; Pred. No. 0.17;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| | | | | | | |  
Db 161 EADPTGHSY 169

RESULT 9

US-11-371-354-73367  
; Sequence 73367, Application US/11371354



```

; GENERAL INFORMATION:
; APPLICANT: CARRINO, JOHN
; APPLICANT: LIANG, FENG
; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS
; FILE REFERENCE: INV-1005-UT2
; CURRENT APPLICATION NUMBER: US/11/371,354
; CURRENT FILING DATE: 2006-03-07
; PRIOR APPLICATION NUMBER: 60/673,045
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/665,199
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/665,200
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/659,493
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/659,492
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/953,586
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/651,390
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 78682
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73367
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-371-354-73367

```

```

Query Match          84.6%; Score 44; DB 7; Length 369;
Best Local Similarity 77.8%; Pred. No. 1.4;
Matches      7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 EADPTGHSY 9
        | | | | | :
Db      193 EVDPTGHSF 201

```

```

RESULT 10
US-11-371-354-69197
; Sequence 69197, Application US/11371354
; GENERAL INFORMATION:
; APPLICANT: CARRINO, JOHN
; APPLICANT: LIANG, FENG
; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS
; FILE REFERENCE: INV-1005-UT2
; CURRENT APPLICATION NUMBER: US/11/371,354
; CURRENT FILING DATE: 2006-03-07
; PRIOR APPLICATION NUMBER: 60/673,045
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/665,199
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/665,200
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/659,493
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/659,492
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/953,586

```

; PRIOR FILING DATE: 2005-02-15  
; PRIOR APPLICATION NUMBER: 60/651,390  
; PRIOR FILING DATE: 2005-02-08  
; NUMBER OF SEQ ID NOS: 78682  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 69197  
; LENGTH: 315  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-371-354-69197

Query Match 82.7%; Score 43; DB 7; Length 315;  
Best Local Similarity 77.8%; Pred. No. 1.9;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| || ||||  
Db 167 EVDPAGHSY 175

RESULT 11

US-11-371-354-71659  
; Sequence 71659, Application US/11371354  
; GENERAL INFORMATION:  
; APPLICANT: CARRINO, JOHN  
; APPLICANT: LIANG, FENG  
; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR  
; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS  
; FILE REFERENCE: INV-1005-UT2  
; CURRENT APPLICATION NUMBER: US/11/371,354  
; CURRENT FILING DATE: 2006-03-07  
; PRIOR APPLICATION NUMBER: 60/673,045  
; PRIOR FILING DATE: 2005-04-19  
; PRIOR APPLICATION NUMBER: 60/665,199  
; PRIOR FILING DATE: 2005-03-25  
; PRIOR APPLICATION NUMBER: 60/665,200  
; PRIOR FILING DATE: 2005-03-25  
; PRIOR APPLICATION NUMBER: 60/659,493  
; PRIOR FILING DATE: 2005-03-07  
; PRIOR APPLICATION NUMBER: 60/659,492  
; PRIOR FILING DATE: 2005-03-07  
; PRIOR APPLICATION NUMBER: 60/953,586  
; PRIOR FILING DATE: 2005-02-15  
; PRIOR APPLICATION NUMBER: 60/651,390  
; PRIOR FILING DATE: 2005-02-08  
; NUMBER OF SEQ ID NOS: 78682  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 71659  
; LENGTH: 318  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-371-354-71659

Query Match 82.7%; Score 43; DB 7; Length 318;  
Best Local Similarity 77.8%; Pred. No. 1.9;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| || ||||  
Db 171 EVDPAGHSY 179

RESULT 12  
 US-11-371-354-73341  
 ; Sequence 73341, Application US/11371354  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARRINO, JOHN  
 ; APPLICANT: LIANG, FENG  
 ; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR  
 ; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS  
 ; FILE REFERENCE: INV-1005-UT2  
 ; CURRENT APPLICATION NUMBER: US/11/371,354  
 ; CURRENT FILING DATE: 2006-03-07  
 ; PRIOR APPLICATION NUMBER: 60/673,045  
 ; PRIOR FILING DATE: 2005-04-19  
 ; PRIOR APPLICATION NUMBER: 60/665,199  
 ; PRIOR FILING DATE: 2005-03-25  
 ; PRIOR APPLICATION NUMBER: 60/665,200  
 ; PRIOR FILING DATE: 2005-03-25  
 ; PRIOR APPLICATION NUMBER: 60/659,493  
 ; PRIOR FILING DATE: 2005-03-07  
 ; PRIOR APPLICATION NUMBER: 60/659,492  
 ; PRIOR FILING DATE: 2005-03-07  
 ; PRIOR APPLICATION NUMBER: 60/953,586  
 ; PRIOR FILING DATE: 2005-02-15  
 ; PRIOR APPLICATION NUMBER: 60/651,390  
 ; PRIOR FILING DATE: 2005-02-08  
 ; NUMBER OF SEQ ID NOS: 78682  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 73341  
 ; LENGTH: 319  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-371-354-73341

Query Match 80.8%; Score 42; DB 7; Length 319;  
 Best Local Similarity 77.8%; Pred. No. 2.9;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
 | | | | |  
 Db 171 EVDPTSHSY 179

RESULT 13  
 US-10-669-920-860  
 ; Sequence 860, Application US/10669920  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Morris, David W.  
 ; APPLICANT: Malandro, Marc S.  
 ; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER  
 ; FILE REFERENCE: 20366-066001  
 ; CURRENT APPLICATION NUMBER: US/10/669,920  
 ; CURRENT FILING DATE: 2003-09-23  
 ; PRIOR APPLICATION NUMBER: US 10/004,113  
 ; PRIOR FILING DATE: 2001-10-23  
 ; PRIOR APPLICATION NUMBER: US 10/052,482  
 ; PRIOR FILING DATE: 2001-11-08  
 ; PRIOR APPLICATION NUMBER: US 09/997,722  
 ; PRIOR FILING DATE: 2001-11-30  
 ; PRIOR APPLICATION NUMBER: US 10/034,650  
 ; PRIOR FILING DATE: 2001-12-20

```

; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 860
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-669-920-860

```

```

Query Match          71.2%; Score 37; DB 6; Length 1049;
Best Local Similarity 100.0%; Pred. No. 91;
Matches      6; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      4 PTGHSY 9
        |||||
Db      52 PTGHSY 57

```

```

RESULT 14
US-10-362-715A-12
; Sequence 12, Application US/10362715A
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: Schuler-Thurner, Beatrice
; TITLE OF INVENTION: METHOD FOR READY-TO-USE, ANTIGEN LOADED OR UNLOADED,
; TITLE OF INVENTION: CRYOCONSERVED MATURE DENDRITIC CELLS
; FILE REFERENCE: ARG015
; CURRENT APPLICATION NUMBER: US/10/362,715A
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09790
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 10041515.6
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-715A-12

```

```

Query Match          69.2%; Score 36; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 3.2e+05;
Matches      6; Conservative      0; Mismatches      3; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EVDPIGHLI 9

```

```

RESULT 15
US-10-362-715A-23
; Sequence 23, Application US/10362715A
; GENERAL INFORMATION:

```

```

; APPLICANT: Schuler, Gerold
; APPLICANT: Schuler-Thurner, Beatrice
; TITLE OF INVENTION: METHOD FOR READY-TO-USE, ANTIGEN LOADED OR UNLOADED,
; TITLE OF INVENTION: CRYOCONSERVED MATURE DENDRITIC CELLS
; FILE REFERENCE: ARG015
; CURRENT APPLICATION NUMBER: US/10/362,715A
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09790
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 10041515.6
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-715A-23

```

```

Query Match          69.2%; Score 36; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 1;
Matches      6; Conservative    0; Mismatches    3; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        | | | | |
Db      2 EVDPIGHLy 10

```

Search completed: August 25, 2006, 01:12:05  
Job time : 41 secs

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SCORE 1.3 BuildDate: 12/06/2005

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This page gives you Search Results detail for the Application 08819669 and Search Result us-08-81 start

A;Cross-references: UNIPROT:Q10635; UNIPARC:UPI000013A7EA; GB:Z73902; GB:AL123456; NID  
 Caulobacter crescentus C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-J  
 White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4  
 Query Match 67.3%; Score 35; DB 2; Length 385; Best Local Similarity 66.7%; Pred. No. 60; Matc

GenCore version 5.1.9  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2006, 00:54:42 ; Search time 39 Seconds  
 (without alignments)  
 22.204 Million cell updates/sec

Title: US-08-819-669E-26  
 Perfect score: 52  
 Sequence: 1 EADPTGHSY 9

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_80:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	52	100.0	280	2	JC2358	melanoma antigen M
2	44	84.6	369	2	I38659	melanoma antigen M
3	43	82.7	234	2	I38667	melanoma antigen M

4	43	82.7	315	2	I38668	melanoma antigen M
5	42	80.8	319	2	I38660	melanoma antigen M
6	38	73.1	129	2	E72685	hypothetical prote
7	38	73.1	305	2	H83287	conserved hypothet
8	37	71.2	555	1	RGASWA	regulatory protein
9	36	69.2	133	2	I38663	melanoma antigen M
10	36	69.2	314	2	JC2360	melanoma antigen M
11	36	69.2	314	2	JC2361	melanoma antigen M
12	36	69.2	1375	2	T37672	probable DNA repai
13	36	69.2	3396	1	A42551	genome polyprotein
14	35	67.3	98	2	F70769	hypothetical prote
15	35	67.3	385	2	B87441	rod shape-determin
16	35	67.3	428	2	AD2938	hypothetical prote
17	35	67.3	430	2	C98344	sugar-binding prot
18	35	67.3	925	1	A39216	nucleotide diphosp
19	35	67.3	1033	2	S02168	type I site-specif
20	35	67.3	1187	2	T31351	endo-1,4-beta-xyla
21	34	65.4	197	2	A70832	hypothetical prote
22	34	65.4	215	2	T35768	hypothetical prote
23	34	65.4	224	2	T34937	hypothetical prote
24	34	65.4	322	2	AH1348	oligopeptide ABC t
25	34	65.4	370	2	S49008	fork head protein
26	34	65.4	497	1	S33938	penton protein (II
27	34	65.4	668	2	T18635	hypothetical prote
28	34	65.4	749	2	H82691	topoisomerase IV s
29	34	65.4	878	2	S44543	hypothetical prote
30	34	65.4	1184	2	T09484	cartilage intermed
31	34	65.4	1670	2	S71551	DNA-directed DNA p
32	34	65.4	3942	2	T42730	Bassoon protein -
33	33	63.5	214	2	AH0308	conserved hypothet
34	33	63.5	246	2	T51967	proteasome endopep
35	33	63.5	288	2	A56279	carbon-monoxide de
36	33	63.5	295	2	C69180	adhesion protein -
37	33	63.5	299	2	H82907	pseudouridine synt
38	33	63.5	301	2	C71194	hypothetical prote
39	33	63.5	341	2	T07148	G-box binding fact
40	33	63.5	372	2	S32581	lignin peroxidase
41	33	63.5	388	2	C90059	3-hydroxy-3-methyl
42	33	63.5	457	2	T39751	major facilitator
43	33	63.5	488	1	A53107	sulfite oxidase (E
44	33	63.5	488	1	S55874	sulfite oxidase (E
45	33	63.5	597	1	S37849	DNA intrastrand cr

#### ALIGNMENTS

##### RESULT 1

JC2358

melanoma antigen MAGE-1 - human

C;Species: Homo sapiens (man)

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 18-Feb-2000

C;Accession: JC2358

R;Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.

Biochem. Biophys. Res. Commun. 202, 549-555, 1994

A;Title: Cloning and analysis of MAGE-1-related genes.

A;Reference number: JC2358; MUID:94311935; PMID:8037761

A;Accession: JC2358

A;Molecule type: mRNA

A;Residues: 1-280

A;Cross-references: UNIPARC:UPI0000178982

A;Experimental source: melanoma cell line DM150  
C;Genetics:  
A;Gene: MAGE  
C;Superfamily: tumor associated protein MAGE  
F;161-169/Region: HLA-A1 binding #status predicted

Query Match 100.0%; Score 52; DB 2; Length 280;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| | | | | | | | |  
Db 161 EADPTGHSY 169

RESULT 2

I38659

melanoma antigen MAGE-10 - human

C;Species: Homo sapiens (man)

C;Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 09-Jul-2004

C;Accession: I38659

R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.;  
Immunogenetics 40, 360-369, 1994

A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE f

A;Reference number: I38659; MUID:95012457; PMID:7927540

A;Accession: I38659

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-369

A;Cross-references: UNIPROT:P43363; UNIPARC:UPI0000000C57; EMBL:U10685; NID:g533510; P

C;Genetics:

A;Gene: GDB:MAGEA10; MAGE10

A;Cross-references: GDB:331126

A;Map position: Xq28-Xq28

A;Introns: #status absent

C;Superfamily: tumor associated protein MAGE

Query Match 84.6%; Score 44; DB 2; Length 369;  
Best Local Similarity 77.8%; Pred. No. 1.1;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| | | | | | | | |  
Db 193 EVDPTGHSF 201

RESULT 3

I38667

melanoma antigen MAGE-8 - human

C;Species: Homo sapiens (man)

C;Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 09-Jul-2004

C;Accession: I38667

R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.;  
Immunogenetics 40, 360-369, 1994

A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE f

A;Reference number: I38659; MUID:95012457; PMID:7927540

A;Accession: I38667

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-234

A;Cross-references: UNIPROT:P43361; UNIPARC:UPI00000335D6; EMBL:U10693; NID:g533525; P



C;Genetics:  
A;Gene: GDB:MAGEA8; MAGE8  
A;Cross-references: GDB:331123  
A;Map position: Xq28-Xq28  
A;Introns: #status absent  
C;Superfamily: tumor associated protein MAGE

Query Match 82.7%; Score 43; DB 2; Length 234;  
Best Local Similarity 77.8%; Pred. No. 1;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| || ||||  
Db 171 EVDPAGHSY 179

RESULT 4  
I38668

melanoma antigen MAGE-9 - human  
C;Species: Homo sapiens (man)  
C;Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 09-Jul-2004  
C;Accession: I38668  
R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.;  
Immunogenetics 40, 360-369, 1994  
A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE f  
A;Reference number: I38659; MUID:95012457; PMID:7927540  
A;Accession: I38668  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-315  
A;Cross-references: UNIPROT:P43362; UNIPARC:UPI000012EB2B; EMBL:U10694; NID:g533527; P  
C;Genetics:  
A;Gene: GDB:MAGEA9; MAGE9  
A;Cross-references: GDB:331125  
A;Map position: Xp21.3-Xp21.3  
A;Introns: #status absent  
C;Superfamily: tumor associated protein MAGE

Query Match 82.7%; Score 43; DB 2; Length 315;  
Best Local Similarity 77.8%; Pred. No. 1.4;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| || ||||  
Db 167 EVDPAGHSY 175

RESULT 5  
I38660

melanoma antigen MAGE-11 - human  
C;Species: Homo sapiens (man)  
C;Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 09-Jul-2004  
C;Accession: I38660  
R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.;  
Immunogenetics 40, 360-369, 1994  
A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE f  
A;Reference number: I38659; MUID:95012457; PMID:7927540  
A;Accession: I38660  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-319

A;Cross-references: UNIPROT:P43364; UNIPARC:UPI0000000C62; EMBL:U10686; NID:g533512; P  
C;Genetics:  
A;Gene: GDB:MAGEA11; MAGE11  
A;Cross-references: GDB:331128  
A;Map position: Xq28-Xq28  
A;Introns: #status absent  
C;Superfamily: tumor associated protein MAGE

Query Match 80.8%; Score 42; DB 2; Length 319;  
Best Local Similarity 77.8%; Pred. No. 2.2;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| ||| |||  
Db 171 EVDPTSHSY 179

#### RESULT 6

E72685

hypothetical protein APE0901 - Aeropyrum pernix (strain K1)

C;Species: Aeropyrum pernix

C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004

C;Accession: E72685

R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tak  
DNA Res. 6, 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aerop

A;Reference number: A72450; MUID:99310339; PMID:10382966

A;Accession: E72685

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-129

A;Cross-references: UNIPROT:Q9YDL2; UNIPARC:UPI000005DD2A; DDBJ:AP000060; NID:g5104188

A;Experimental source: strain K1

C;Genetics:

A;Gene: APE0901

C;Superfamily: Aeropyrum pernix hypothetical protein APE0901

Query Match 73.1%; Score 38; DB 2; Length 129;  
Best Local Similarity 85.7%; Pred. No. 4.9;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 DPTGHSY 9  
|| ||||  
Db 115 DPAGHSY 121

#### RESULT 7

H83287

conserved hypothetical protein PA2875 [imported] - Pseudomonas aeruginosa (strain PA01

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004

C;Accession: H83287

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;  
Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat

A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: H83287

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-305

A;Cross-references: UNIPROT:Q9HZX1; UNIPARC:UPI00000C5857; GB:AE004713; GB:AE004091; N

A;Experimental source: strain PAO1  
C;Genetics:  
A;Gene: PA2875  
C;Superfamily: methanol dehydrogenase regulatory protein

Query Match 73.1%; Score 38; DB 2; Length 305;  
Best Local Similarity 85.7%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGH 7  
:|||||  
Db 283 QADPTGH 289

RESULT 8

RGASWA

regulatory protein wetA - Emericella nidulans

C;Species: Emericella nidulans, Aspergillus nidulans

C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004

C;Accession: A39665

R;Marshall, M.A.; Timberlake, W.E.

Mol. Cell. Biol. 11, 55-62, 1991

A;Title: Aspergillus nidulans wetA activates spore-specific gene expression.

A;Reference number: A39665; MUID:91094871; PMID:1986246

A;Accession: A39665

A;Molecule type: DNA

A;Residues: 1-555

A;Cross-references: UNIPROT:P22022; UNIPARC:UPI0000138EF8; GB:M60528; GB:M35758; NID:g

C;Comment: The products of the genes brlA, abaA, and wetA are required for activation

C;Genetics:

A;Gene: wetA

C;Superfamily: regulatory protein wetA

C;Keywords: transcription regulation

Query Match 71.2%; Score 37; DB 1; Length 555;  
Best Local Similarity 87.5%; Pred. No. 37;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EADPTGHS 8  
||| |||  
Db 109 EADATGHS 116

RESULT 9

I38663

melanoma antigen MAGE-5 - human (fragments)

C;Species: Homo sapiens (man)

C;Date: 07-Jun-1996 #sequence\_revision 18-Feb-2000 #text\_change 09-Jul-2004

C;Accession: I38663; I38664; PH1299; PH1300

R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Immunogenetics 40, 360-369, 1994

A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE f

A;Reference number: I38659; MUID:95012457; PMID:7927540

A;Accession: I38663

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-124

A;Cross-references: UNIPROT:P43359; UNIPARC:UPI000012EB2A; EMBL:U10689; NID:g533518; P

A;Experimental source: MAGE-5a antigen

A;Accession: I38664

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA  
 A;Residues: 1-124  
 A;Cross-references: UNIPARC:UPI000012EB2A; EMBL:U10690; NID:g533520; PIDN:AAA68874.1;  
 A;Experimental source: MAGE-5b antigen  
 A;Note: these sequences seem to be incomplete with respect to other members of the sup  
 R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pe  
 J. Exp. Med. 176, 1453-1457, 1992  
 A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolyt  
 A;Reference number: PH1294; MUID:93018875; PMID:1402688  
 A;Accession: PH1299  
 A;Molecule type: DNA  
 A;Residues: 125-133  
 A;Cross-references: UNIPARC:UPI0000042533  
 A;Experimental source: MAGE 5 protein  
 A;Accession: PH1300  
 A;Molecule type: DNA  
 A;Residues: 125-133  
 A;Cross-references: UNIPARC:UPI0000042533  
 A;Experimental source: MAGE 5l protein  
 C;Genetics:  
 A;Gene: GDB:MAGEA5; MAGE5  
 A;Cross-references: GDB:331120  
 A;Map position: Xq28-Xq28  
 A;Introns: #status absent  
 C;Superfamily: tumor associated protein MAGE

Query Match 69.2%; Score 36; DB 2; Length 133;  
 Best Local Similarity 66.7%; Pred. No. 12;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EADPTGHSY 9  
 ||||| ::|  
 Db 125 EADPTSNTY 133

RESULT 10  
 JC2360  
 melanoma antigen MAGE-6 - human  
 N;Alternate names: tumor-associated antigen, MAGE-3b  
 C;Species: Homo sapiens (man)  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
 C;Accession: JC2360; PH1301; I38665; G01445  
 R;Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.  
 Biochem. Biophys. Res. Commun. 202, 549-555, 1994  
 A;Title: Cloning and analysis of MAGE-1-related genes.  
 A;Reference number: JC2358; MUID:94311935; PMID:8037761  
 A;Accession: JC2360  
 A;Molecule type: mRNA  
 A;Residues: 1-314  
 A;Cross-references: UNIPROT:P43360; UNIPARC:UPI000000D9B0  
 A;Experimental source: melanoma cell line DM150  
 R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pe  
 J. Exp. Med. 176, 1453-1457, 1992  
 A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolyt  
 A;Reference number: PH1294; MUID:93018875; PMID:1402688  
 A;Accession: PH1301  
 A;Molecule type: DNA  
 A;Residues: 168-176  
 A;Cross-references: UNIPARC:UPI0000042625  
 R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.;  
 Immunogenetics 40, 360-369, 1994

A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE f  
 A;Reference number: I38659; MUID:95012457; PMID:7927540  
 A;Accession: I38665  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-314  
 A;Cross-references: UNIPARC:UPI000000D9B0; EMBL:U10691; NID:g533522; PIDN:AAA68875.1;  
 R;Fenton, R.G.  
 submitted to the EMBL Data Library, June 1994  
 A;Reference number: G07126  
 A;Accession: G01445  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-314  
 A;Cross-references: UNIPARC:UPI000000D9B0; EMBL:U10339; NID:g499121; PIDN:AAA19006.1;  
 C;Genetics:  
 A;Gene: GDB:MAGEA6; MAGE6  
 A;Cross-references: GDB:331121  
 A;Map position: Xq28-Xq28  
 A;Introns: #status absent  
 C;Superfamily: tumor associated protein MAGE  
 F;168-176/Region: HLA-A1 binding #status predicted

Query Match 69.2%; Score 36; DB 2; Length 314;  
 Best Local Similarity 66.7%; Pred. No. 31;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EADPTGHSY 9  
 | | | | |  
 Db 168 EVDPIGHVY 176

# RESULT 11

JC2361

melanoma antigen MAGE-3 - human

N;Alternate names: MAGE 3 protein

C;Species: Homo sapiens (man)

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C;Accession: JC2361; PH1296; I38438

R;Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.

Biochem. Biophys. Res. Commun. 202, 549-555, 1994

A;Title: Cloning and analysis of MAGE-1-related genes.

A;Reference number: JC2358; MUID:94311935; PMID:8037761

A;Accession: JC2361

A;Molecule type: mRNA

A;Residues: 1-314

A;Cross-references: UNIPROT:P43357; UNIPARC:UPI0000062194

A;Experimental source: melanoma cell line DM150

R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pe  
 J. Exp. Med. 176, 1453-1457, 1992

A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolyt

A;Reference number: PH1294; MUID:93018875; PMID:1402688

A;Accession: PH1296

A;Molecule type: DNA

A;Residues: 168-176

A;Cross-references: UNIPARC:UPI000002F152

R;Gaugler, B.; Van den Eynde, B.; van der Bruggen, P.; Romero, P.; Gaforio, J.J.; De P  
 J. Exp. Med. 179, 921-930, 1994

A;Title: Human gene MAGE-3 codes for an antigen recognized on a melanoma by autologous

A;Reference number: I38438; MUID:94157413; PMID:8113684

A;Accession: I38438

A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-314  
A;Cross-references: UNIPARC:UPI0000062194; EMBL:U03735; NID:g468825; PIDN:AAA17446.1;  
C;Genetics:  
A;Gene: MAGE-3  
C;Superfamily: tumor associated protein MAGE  
F;168-176/Region: HLA-A1 binding #status predicted

Query Match 69.2%; Score 36; DB 2; Length 314;  
Best Local Similarity 66.7%; Pred. No. 31;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| || || |  
Db 168 EVDPIGHLY 176

#### RESULT 12

T37672

probable DNA repair protein - fission yeast (*Schizosaccharomyces pombe*)  
C;Species: *Schizosaccharomyces pombe*  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T37672  
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Davis, P.; Churcher, C.M.  
submitted to the EMBL Data Library, October 1999  
A;Reference number: Z21736  
A;Accession: T37672  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-1375  
A;Cross-references: UNIPROT:Q9UTL9; UNIPARC:UPI0000069886; EMBL:AL132675; PIDN:CAB5968  
A;Experimental source: strain 972h-; cosmid c144  
C;Genetics:  
A;Gene: SPDB:SPAC144.05  
A;Map position: 1  
A;Introns: 1108/1; 1196/3; 1263/2; 1277/1  
F;1088-1135/Domain: RING finger homology

Query Match 69.2%; Score 36; DB 2; Length 1375;  
Best Local Similarity 66.7%; Pred. No. 1.5e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
|:|||| |  
Db 810 ESDPTGDEY 818

#### RESULT 13

A42551

genome polyprotein - dengue virus type 1 (strain Singapore S275/90)  
N;Contains: capsid protein; envelope protein; membrane protein; nonstructural protein  
C;Species: dengue virus type 1  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 31-Dec-2004  
C;Accession: A42551  
R;Fu, J.; Tan, B.H.; Yap, E.H.; Chan, Y.C.; Tan, Y.H.  
Virology 188, 953-958, 1992  
A;Title: Full-length cDNA sequence of dengue type 1 virus (Singapore strain S275/90).  
A;Reference number: A42551; MUID:92263809; PMID:1585663  
A;Accession: A42551  
A;Molecule type: genomic RNA

A;Residues: 1-3396  
 A;Cross-references: UNIPROT:P33478; UNIPARC:UPI000002F845; GB:M87512  
 C;Superfamily: hepatitis C virus genome polyprotein  
 C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein  
 F;1-114/Product: capsid protein #status predicted  
 F;115-281/Product: membrane protein precursor #status predicted  
 F;115-204/Domain: nonterminal signal sequence #status predicted  
 F;205-281/Product: membrane protein #status predicted  
 F;267-279/Domain: transmembrane #status predicted  
 F;282-774/Product: envelope protein #status predicted  
 F;753-769/Domain: transmembrane #status predicted  
 F;775-1127/Product: nonstructural protein NS1 #status predicted  
 F;1128-1344/Product: nonstructural protein NS2a #status predicted  
 F;1345-1474/Product: nonstructural protein NS2b #status predicted  
 F;1475-2093/Product: nonstructural protein NS3 #status predicted  
 F;1668-1675/Region: nucleotide-binding motif A (P-loop)  
 F;1755-1760/Region: nucleotide-binding motif B  
 F;1759-1762/Region: DEAH motif  
 F;2094-2243/Product: nonstructural protein NS4a #status predicted  
 F;2244-2492/Product: nonstructural protein NS4b #status predicted  
 F;2493-3396/Product: nonstructural protein NS5 #status predicted  
 F;183,347,433/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 69.2%; Score 36; DB 1; Length 3396;  
 Best Local Similarity 75.0%; Pred. No. 4e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EADPTGHS 8  
 . |:|| |||  
 Db 3383 ESDPKGHS 3390

#### RESULT 14

F70769

hypothetical protein Rv1322 - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004

C;Accession: F70769

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Nature 393, 537-544, 1998

A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: F70769

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-98

# SCORE Search Results Details for Application 08819669 and Search Result us-08-819-669e- 26.rup.

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OM protein - protein search, using sw model

Run on: August 25, 2006, 00:51:11 ; Search time 299 Seconds  
(without alignments)  
27.843 Million cell updates/sec

Title: US-08-819-669E-26  
Perfect score: 52  
Sequence: 1 EADPTGHSY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	52	100.0	309	1	MAGA1_HUMAN	P43355 homo sapien
2	44	84.6	369	1	MAGAA_HUMAN	P43363 homo sapien
3	43	82.7	234	1	MAGA8_HUMAN	P43361 homo sapien
4	43	82.7	315	1	MAGA9_HUMAN	P43362 homo sapien



5	43	82.7	315	2	Q7Z5K4_HUMAN	Q7z5k4	homo sapien
6	43	82.7	318	2	Q9BUN9_HUMAN	Q9bun9	homo sapien
7	42	80.8	319	1	MAGAB_HUMAN	P43364	homo sapien
8	42	80.8	394	2	Q6ZRZ5_HUMAN	Q6zrz5	homo sapien
9	42	80.8	429	2	Q5ETU4_HUMAN	Q5etu4	homo sapien
10	40	76.9	259	1	PYRK_BACAN	Q81wf3	bacillus an
11	40	76.9	259	1	PYRK_BACCR	Q819s4	bacillus ce
12	40	76.9	259	2	Q3ENC9_BACTI	Q3enc9	bacillus th
13	40	76.9	259	2	Q4MJ43_BACCE	Q4mj43	bacillus ce
14	40	76.9	259	2	Q636E1_BACCZ	Q636e1	bacillus ce
15	40	76.9	259	2	Q6HES9_BACHK	Q6hes9	bacillus th
16	40	76.9	259	2	Q732I4_BACCL	Q732i4	bacillus ce
17	40	76.9	5094	2	Q2IZL4_RHOPA	Q2izl4	rhodopseudo
18	39	75.0	652	2	Q7SDF4_NEUCR	Q7sdf4	neurospora
19	39	75.0	1429	2	Q6CH67_YARLI	Q6ch67	yarrowia li
20	38	73.1	129	2	Q9YDL2_AERPE	Q9ydl2	aeropyrum p
21	38	73.1	130	2	Q825J6_STRAW	Q825j6	streptomyce
22	38	73.1	294	2	Q40M96_DESAC	Q40m96	desulfuromo
23	38	73.1	305	2	Q9HZX1_PSEAE	Q9hzx1	pseudomonas
24	38	73.1	337	2	Q4HXP0_GIBZE	Q4hxp0	gibberella
25	38	73.1	346	2	Q7RXH4_NEUCR	Q7rxh4	neurospora
26	38	73.1	355	2	Q475K8_RALEJ	Q475k8	ralstonia e
27	38	73.1	356	2	Q43QJ8_SOLUS	Q43qj8	solibacter
28	38	73.1	1001	2	Q4PBD5_USTMA	Q4pbd5	ustilago ma
29	38	73.1	1034	2	Q55XT8_CRYNE	Q55xt8	cryptococcu
30	38	73.1	1065	2	Q4PC22_USTMA	Q4pc22	ustilago ma
31	38	73.1	1085	2	Q755J0_ASHGO	Q755j0	ashbya goss
32	37	71.2	86	2	Q61989_MOUSE	Q61989	mus musculu
33	37	71.2	125	2	Q4L989_STAHJ	Q4l989	staphylococ
34	37	71.2	247	2	Q67RX7_SYMTH	Q67rx7	symbiobacte
35	37	71.2	249	2	Q5V7C7_HALMA	Q5v7c7	haloarcula
36	37	71.2	271	2	Q6MHS7_BDEBA	Q6mhs7	bdellovibri
37	37	71.2	279	2	Q3W747_9ACTO	Q3w747	frankia sp.
38	37	71.2	345	2	Q89L61_BRAJA	Q89l61	bradyrhizob
39	37	71.2	479	2	Q4NIV6_9MICC	Q4niv6	arthrobacte
40	37	71.2	555	1	WETA_EMENI	P22022	emericella
41	37	71.2	555	2	Q5BBZ3_EMENI	Q5bbz3	aspergillus
42	37	71.2	604	2	Q3U1F2_MOUSE	Q3ulf2	mus musculu
43	37	71.2	604	2	Q8BQ25_MOUSE	Q8bq25	mus musculu
44	37	71.2	622	1	PFA3_NEUCR	Q7s7c5	neurospora
45	37	71.2	642	2	Q3U0V9_MOUSE	Q3u0v9	mus musculu

#### ALIGNMENTS

##### RESULT 1

##### MAGA1\_HUMAN

ID MAGA1\_HUMAN STANDARD; PRT; 309 AA.  
AC P43355; O00346;  
DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.  
DT 01-NOV-1995, sequence version 1.  
DT 07-FEB-2006, entry version 44.  
DE Melanoma-associated antigen 1 (MAGE-1 antigen) (Antigen MZ2-E).  
GN Name=MAGEA1; Synonyms=MAGE1, MAGE1A;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=92086861; PubMed=1840703;  
RA van der Bruggen P., Traversari C., Chomez P., Lurquin C., de Plaen E.,  
RA van den Eynde B., Knuth A., Boon T.;  
RT "A gene encoding an antigen recognized by cytolytic T lymphocytes on a  
RT human melanoma.";  
RL Science 254:1643-1647(1991).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Skin;  
RX MEDLINE=94311935; PubMed=8037761;  
RA Ding M., Beck R.J., Keller C.J., Fenton R.G.;  
RT "Cloning and analysis of MAGE-1-related genes.";  
RL Biochem. Biophys. Res. Commun. 202:549-555(1994).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX MEDLINE=20314869; PubMed=10854409; DOI=10.1101/gr.10.6.758;  
RA Mallon A.-M., Platzner M., Bate R., Gloeckner G., Botcherby M.R.M.,  
RA Nordsiek G., Strivens M.A., Kioschis P., Dangel A., Cunningham D.,  
RA Straw R.N.A., Weston P., Gilbert M., Fernando S., Goodall K.,  
RA Hunter G., Greyststrong J.S., Clarke D., Kimberley C., Goerdes M.,  
RA Blechschmidt K., Rump A., Hinzmann B., Mundy C.R., Miller W.,  
RA Poustka A., Herman G.E., Rhodes M., Denny P., Rosenthal A.,  
RA Brown S.D.M.;  
RT "Comparative genome sequence analysis of the Bpa/Str region in mouse  
RT and man.";  
RL Genome Res. 10:758-775(2000).  
RN [4]  
RP NUCLEOTIDE SEQUENCE, AND VARIANT ALA-32.  
RA Chen H., Wang L., Mei M., Qin L., Cong X., Xu J., Wei L., Wang Y.,  
RA Chen W.;  
RT "The polymorphism of MAGE-1 gene in Chinese people.";  
RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.  
RN [5]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT ALA-32.  
RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,  
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,  
RA Phelan M., Farmer A.;  
RT "Cloning of human full-length CDSs in BD Creator(TM) system donor  
RT vector.";  
RL Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.  
RN [6]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT ALA-32.  
RC TISSUE=Skin;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [7]  
 RP MUTAGENESIS.  
 RC TISSUE=Blood;  
 RX MEDLINE=94157413; PubMed=8113684; DOI=10.1084/jem.179.3.921;  
 RA Gaugler B., van den Eynde B., van der Bruggen P., Romero P.,  
 RA Gaforio J.J., de Plaen E., Lethe B., Brasseur F., Boon T.;  
 RT "Human gene MAGE-3 codes for an antigen recognized on a melanoma by  
 RT autologous cytolytic T lymphocytes."  
 RL J. Exp. Med. 179:921-930(1994).  
 RN [8]  
 RP SUBCELLULAR LOCATION.  
 RX MEDLINE=95012905; PubMed=7927954;  
 RA Schultz-Thater E., Juretic A., Dellabona P., Luscher U., Siegrist W.,  
 RA Harder F., Heberer M., Zuber M., Spagnoli G.C.;  
 RT "MAGE-1 gene product is a cytoplasmic protein."  
 RL Int. J. Cancer 59:435-439(1994).  
 CC -!- FUNCTION: Not known, though may play a role in embryonal  
 CC development and tumor transformation or aspects of tumor  
 CC progression. Antigen recognized on a melanoma by autologous  
 CC cytolytic T lymphocytes.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasm.  
 CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,  
 CC such as melanoma, head and neck squamous cell carcinoma, lung  
 CC carcinoma and breast carcinoma, but not in normal tissues except  
 CC for testes. Never expressed in kidney tumors, leukemias and  
 CC lymphomas.  
 CC -!- SIMILARITY: Contains 1 MAGE domain.  
 CC -----  
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 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 DR EMBL; M77481; AAA03229.1; -; Unassigned\_DNA.  
 DR EMBL; U82670; -; NOT\_ANNOTATED\_CDS; Genomic\_DNA.  
 DR EMBL; AY148486; AAN62752.1; -; mRNA.  
 DR EMBL; BT009789; AAP88791.1; -; mRNA.  
 DR EMBL; BC017555; AAH17555.1; -; mRNA.  
 DR PDB; 1W72; X-ray; C/F=161-169.  
 DR Ensembl; ENSG00000126977; Homo sapiens.  
 DR H-InvDB; HIX0017126; -.  
 DR HGNC; HGNC:6796; MAGEA1.  
 DR MIM; 300016; gene.  
 DR GO; GO:0005886; C:plasma membrane; TAS.  
 DR InterPro; IPR002190; MAGE.  
 DR PANTHER; PTHR11736; MAGE; 1.  
 DR Pfam; PF01454; MAGE; 1.  
 DR PROSITE; PS50838; MAGE; 1.  
 KW 3D-structure; Antigen; Polymorphism; Tumor antigen.  
 FT CHAIN 1 309 Melanoma-associated antigen 1.  
 FT /FTId=PRO\_0000156701.  
 FT DOMAIN 102 301 MAGE.  
 FT COMBIAS 33 36 Poly-Ser.  
 FT VARIANT 32 32 T -> A (probable polymorphism).  
 FT /FTId=VAR\_004283.  
 FT VARIANT 72 72 R -> Q (in dbSNP:2008144).  
 FT /FTId=VAR\_011737.  
 FT MUTAGEN 163 163 D->A: Abolishes HLA-A1 binding.  
 FT MUTAGEN 169 169 Y->A: Abolishes HLA-A1 binding.

SQ SEQUENCE 309 AA; 34342 MW; 544EEB1F9F4E9D33 CRC64;

Query Match 100.0%; Score 52; DB 1; Length 309;  
Best Local Similarity 100.0%; Pred. No. 0.29;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| | | | | | | |  
Db 161 EADPTGHSY 169

## RESULT 2

### MAGAA\_HUMAN

ID MAGAA\_HUMAN STANDARD; PRT; 369 AA.  
AC P43363;  
DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.  
DT 01-NOV-1995, sequence version 1.  
DT 07-FEB-2006, entry version 39.  
DE Melanoma-associated antigen 10 (MAGE-10 antigen).  
GN Name=MAGEA10; Synonyms=MAGE10;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=95012457; PubMed=7927540;  
RA de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,  
RA de Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C.,  
RA Brasseur R., Chomez P., de Backer O., Cavenee W., Boon T.;  
RT "Structure, chromosomal localization, and expression of 12 genes of  
RT the MAGE family."  
RL Immunogenetics 40:360-369(1994).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Skin;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Not known, though may play a role in embryonal  
CC development and tumor transformation or aspects of tumor  
CC progression.

CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,  
 CC such as melanoma, head and neck squamous cell carcinoma, lung  
 CC carcinoma and breast carcinoma, but not in normal tissues except  
 CC for testes and placenta.  
 CC -!- SIMILARITY: Contains 1 MAGE domain.  
 CC -----  
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 CC -----  
 DR EMBL; U10685; AAA68869.1; -; Genomic\_DNA.  
 DR EMBL; BC004105; AAH04105.1; -; mRNA.  
 DR PIR; I38659; I38659.  
 DR Ensembl; ENSG00000124260; Homo sapiens.  
 DR H-InvDB; HIX0017116; -.  
 DR HGNC; HGNC:6797; MAGEA10.  
 DR MIM; 300343; gene.  
 DR LinkHub; P43363; -.  
 DR InterPro; IPR002190; MAGE.  
 DR PANTHER; PTHR11736; MAGE; 2.  
 DR Pfam; PF01454; MAGE; 1.  
 DR PROSITE; PS50838; MAGE; 1.  
 KW Antigen; Polymorphism; Tumor antigen.  
 FT CHAIN 1 369 Melanoma-associated antigen 10.  
 FT /FTid=PRO\_0000156709.  
 FT DOMAIN 134 333 MAGE.  
 FT COMPBIAS 54 62 Poly-Ser.  
 FT VARIANT 166 166 K -> R (in dbSNP:210585).  
 FT /FTid=VAR\_024528.  
 SQ SEQUENCE 369 AA; 40767 MW; 16FA3301CAB716A6 CRC64;

Query Match 84.6%; Score 44; DB 1; Length 369;  
 Best Local Similarity 77.8%; Pred. No. 12;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
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 Db 193 EVDPTGHSF 201

RESULT 3  
 MAGA8\_HUMAN  
 ID MAGA8\_HUMAN STANDARD; PRT; 234 AA.  
 AC P43361;  
 DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.  
 DT 01-NOV-1995, sequence version 1.  
 DT 07-FEB-2006, entry version 32.  
 DE Melanoma-associated antigen 8 (MAGE-8 antigen).  
 GN Name=MAGEA8; Synonyms=MAGE8;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RX MEDLINE=95012457; PubMed=7927540;  
 RA de Plaan E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,  
 RA de Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C.,  
 RA Brasseur R., Chomez P., de Backer O., Cavenee W., Boon T.;  
 RT "Structure, chromosomal localization, and expression of 12 genes of  
 RT the MAGE family.";

```

RL   Immunogenetics 40:360-369(1994).
CC   -!- FUNCTION: Not known, though may play a role in embryonal
CC       development and tumor transformation or aspects of tumor
CC       progression.
CC   -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
CC       such as melanoma, head and neck squamous cell carcinoma, lung
CC       carcinoma and breast carcinoma, but not in normal tissues except
CC       for testes and placenta.
CC   -!- SIMILARITY: Contains 1 MAGE domain.
CC   -----
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   -----
DR   EMBL; U10693; AAA68876.1; -; Genomic_DNA.
DR   PIR; I38667; I38667.
DR   Ensembl; ENSG00000156009; Homo sapiens.
DR   HGNC; HGNC:6806; MAGEA8.
DR   MIM; 300341; gene.
DR   InterPro; IPR002190; MAGE.
DR   PANTHER; PTHR11736; MAGE; 1.
DR   Pfam; PF01454; MAGE; 1.
DR   PROSITE; PS50838; MAGE; 1.
KW   Antigen; Tumor antigen.
FT   CHAIN           1      234      Melanoma-associated antigen 8.
FT                                     /FTid=PRO_0000156707.
FT   DOMAIN          112     234     MAGE.
FT   COMPBias         40      43     Poly-Ser.
SQ   SEQUENCE        234 AA;  25197 MW;  058A92EE6003A982 CRC64;

Query Match           82.7%;  Score 43;  DB 1;  Length 234;
Best Local Similarity  77.8%;  Pred. No. 11;
Matches      7;  Conservative    0;  Mismatches    2;  Indels      0;  Gaps      0;

QY           1 EADPTGHSY 9
              | || |||
Db          171 EVDPAGHSY 179

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RESULT 4
MAGA9_HUMAN
ID   MAGA9_HUMAN      STANDARD;          PRT;   315 AA.
AC   P43362; Q92910;
DT   01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1995, sequence version 1.
DT   07-FEB-2006, entry version 37.
DE   Melanoma-associated antigen 9 (MAGE-9 antigen).
GN   Name=MAGEA9; Synonyms=MAGE9;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=95012457; PubMed=7927540;
RA   de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,
RA   de Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C.,
RA   Brasseur R., Chomez P., de Backer O., Cavenne W., Boon T.;
RT   "Structure, chromosomal localization, and expression of 12 genes of
RT   the MAGE family.";
RL   Immunogenetics 40:360-369(1994).

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RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Timms K.M., Bondeson M.L., Ansari-Lari M.A., Lagerstedt K.,  
 RA Nelson D.L., Pettersson U., Gibbs R.A.;  
 RL Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: Not known, though may play a role in embryonal  
 CC development and tumor transformation or aspects of tumor  
 CC progression.  
 CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,  
 CC such as melanoma, head and neck squamous cell carcinoma, lung  
 CC carcinoma and breast carcinoma, but not in normal tissues except  
 CC for testes and placenta.  
 CC -!- SIMILARITY: Contains 1 MAGE domain.  
 CC -----  
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 CC -----  
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 DR EMBL; U66083; AAB67888.1; -; Genomic\_DNA.  
 DR EMBL; BC002351; AAH02351.1; -; mRNA.  
 DR PIR; I38668; I38668.  
 DR H-InvDB; HIX0017105; -.  
 DR HGNC; HGNC:6807; MAGEA9.  
 DR MIM; 300342; gene.  
 DR InterPro; IPR002190; MAGE.  
 DR PANTHER; PTHR11736; MAGE; 1.  
 DR Pfam; PF01454; MAGE; 1.  
 DR PROSITE; PS50838; MAGE; 1.  
 KW Antigen; Tumor antigen.  
 FT CHAIN 1 315 Melanoma-associated antigen 9.  
 FT /FTId=PRO\_0000156708.  
 FT DOMAIN 108 307 MAGE.  
 FT COMBIAS 34 37 Poly-Glu.  
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 SQ SEQUENCE 315 AA; 35088 MW; 7FD2ED10D680D928 CRC64;

Query Match 82.7%; Score 43; DB 1; Length 315;

Best Local Similarity 77.8%; Pred. No. 15;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
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Db 167 EVDPAGHSY 175

RESULT 5

Q7Z5K4\_HUMAN  
ID Q7Z5K4\_HUMAN PRELIMINARY; PRT; 315 AA.  
AC Q7Z5K4;  
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2003, sequence version 1.  
DT 07-FEB-2006, entry version 8.  
DE Melanoma antigen family A 9 (Fragment).  
GN Name=MAGEA9;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;  
RA Zhu J., Feng Z., Guan X.;  
RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.  
CC -----  
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CC -----  
DR EMBL; AY310325; AAP82171.1; -; mRNA.  
DR InterPro; IPR002190; MAGE.  
DR PANTHER; PTHR11736; MAGE; 1.  
DR Pfam; PF01454; MAGE; 1.  
DR PROSITE; PS50838; MAGE; 1.  
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SQ SEQUENCE 315 AA; 35116 MW; C9488470D409B96F CRC64;

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Best Local Similarity 77.8%; Pred. No. 15;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
| || ||||  
Db 167 EVDPAGHSY 175

RESULT 6

Q9BUN9\_HUMAN  
ID Q9BUN9\_HUMAN PRELIMINARY; PRT; 318 AA.  
AC Q9BUN9;  
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.  
DT 01-JUN-2001, sequence version 1.  
DT 07-FEB-2006, entry version 21.  
DE Melanoma antigen family A, 8.  
GN Name=MAGEA8;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.



OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Skin;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Skin;  
 RG NIH MGC Project;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,  
 RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,  
 RA Phelan M., Farmer A.;  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Skin;  
 RA Director MGC Project;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.  
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 CC -----  
 DR EMBL; BC002455; AAH02455.1; -; mRNA.  
 DR EMBL; BT007340; AAP36004.1; -; mRNA.  
 DR EMBL; BC012744; AAH12744.1; -; mRNA.  
 DR Ensembl; ENSG00000156009; Homo sapiens.  
 DR InterPro; IPR002190; MAGE.  
 DR PANTHER; PTHR11736; MAGE; 1.  
 DR Pfam; PF01454; MAGE; 1.  
 DR PROSITE; PS50838; MAGE; 1.  
 SQ SEQUENCE 318 AA; 35215 MW; EA02C1FB42F6C080 CRC64;  
  
 Query Match 82.7%; Score 43; DB 2; Length 318;  
 Best Local Similarity 77.8%; Pred. No. 15;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EADPTGHSY 9  
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RESULT 7

MAGAB\_HUMAN

ID MAGAB\_HUMAN STANDARD; PRT; 319 AA.  
AC P43364;  
DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.  
DT 01-NOV-1995, sequence version 1.  
DT 07-FEB-2006, entry version 36.  
DE Melanoma-associated antigen 11 (MAGE-11 antigen).  
GN Name=MAGEA11; Synonyms=MAGE11;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=95012457; PubMed=7927540;  
RA de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,  
RA de Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C.,  
RA Brasseur R., Chomez P., de Backer O., Cavenee W., Boon T.;  
RT "Structure, chromosomal localization, and expression of 12 genes of  
RT the MAGE family.";  
RL Immunogenetics 40:360-369(1994).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Skin;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Not known, though may play a role in embryonal  
CC development and tumor transformation or aspects of tumor  
CC progression.  
CC -!- INTERACTION:  
CC Q96AJ1:CLUAP1; NbExp=1; IntAct=EBI-739552, EBI-739780;  
CC Q96C88:SH2D4A; NbExp=1; IntAct=EBI-739552, EBI-747035;  
CC Q15560:TCEA2; NbExp=1; IntAct=EBI-739552, EBI-710310;  
CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,  
CC such as melanoma, head and neck squamous cell carcinoma, lung  
CC carcinoma and breast carcinoma, but not in normal tissues except  
CC for testes and placenta.

```

CC  -!- SIMILARITY: Contains 1 MAGE domain.
CC  -----
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CC  -----
DR  EMBL; U10686; AAA68870.1; -; Genomic_DNA.
DR  EMBL; BC004479; AAH04479.1; -; mRNA.
DR  PIR; I38660; I38660.
DR  IntAct; P43364; -.
DR  Ensembl; ENSG00000185247; Homo sapiens.
DR  H-InvDB; HIX0022316; -.
DR  HGNC; HGNC:6798; MAGEA11.
DR  MIM; 300344; gene.
DR  InterPro; IPR002190; MAGE.
DR  PANTHER; PTHR11736; MAGE; 1.
DR  Pfam; PF01454; MAGE; 1.
DR  PROSITE; PS50838; MAGE; 1.
KW  Antigen; Tumor antigen.
FT  CHAIN           1       319       Melanoma-associated antigen 11.
FT                                     /FTId=PRO_0000156710.
FT  DOMAIN          112      311      MAGE.
SQ  SEQUENCE        319 AA;  35536 MW;  F51A0B4140277BE3 CRC64;

Query Match           80.8%;  Score 42;  DB 1;  Length 319;
Best Local Similarity  77.8%;  Pred. No. 24;
Matches      7;  Conservative      0;  Mismatches      2;  Indels      0;  Gaps      0;

Qy          1 EADPTGHSY 9
             | ||| |||
Db          171 EVDPTSHSY 179

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RESULT 8
Q6ZRZ5_HUMAN
ID  Q6ZRZ5_HUMAN  PRELIMINARY;  PRT;  394 AA.
AC  Q6ZRZ5;
DT  05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT  05-JUL-2004, sequence version 1.
DT  21-FEB-2006, entry version 8.
DE  CDNA FLJ45952 fis, clone PLACE7009563, highly similar to Melanoma-
DE  associated antigen 11.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC  Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Placenta;
RA  Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA  Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA  Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA  Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA  Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA  Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA  Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA  Isogai T.;
RT  "NEDO human cDNA sequencing project.";
RL  Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC  -----
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 CC -----  
 DR EMBL; AK127849; BAC87161.1; -; mRNA.  
 DR Ensembl; ENSG00000185247; Homo sapiens.  
 DR LinkHub; Q6ZRZ5; -.  
 DR InterPro; IPR002190; MAGE.  
 DR PANTHER; PTHR11736; MAGE; 1.  
 DR Pfam; PF01454; MAGE; 1.  
 DR PROSITE; PS50838; MAGE; 1.  
 SQ SEQUENCE 394 AA; 44276 MW; 36D7A81D8749D896 CRC64;

Query Match 80.8%; Score 42; DB 2; Length 394;  
 Best Local Similarity 77.8%; Pred. No. 30;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
 | ||| |||  
 Db 246 EVDPTSHSY 254

RESULT 9  
 Q5ETU4\_HUMAN  
 ID Q5ETU4\_HUMAN PRELIMINARY; PRT; 429 AA.  
 AC Q5ETU4;  
 DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.  
 DT 15-MAR-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 4.  
 DE Melanoma antigen family A 11.  
 GN Name=MAGEA11;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Testis;  
 RX PubMed=15684378; DOI=10.1128/MCB.25.4.1238-1257.2005;  
 RA Bai S., He B., Wilson E.M.;  
 RT "Melanoma Antigen Gene Protein MAGE-11 Regulates Androgen Receptor  
 RT Function by Modulating the Interdomain Interaction."  
 RL Mol. Cell. Biol. 25:1238-1257(2005).  
 CC -----  
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 CC -----  
 DR EMBL; AY747607; AAW71787.1; -; mRNA.  
 DR Ensembl; ENSG00000185247; Homo sapiens.  
 DR InterPro; IPR002190; MAGE.  
 DR PANTHER; PTHR11736; MAGE; 1.  
 DR Pfam; PF01454; MAGE; 1.  
 DR PROSITE; PS50838; MAGE; 1.  
 SQ SEQUENCE 429 AA; 48129 MW; FB399ABF47B4C49B CRC64;

Query Match 80.8%; Score 42; DB 2; Length 429;  
 Best Local Similarity 77.8%; Pred. No. 33;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
 | ||| |||  
 Db 281 EVDPTSHSY 289

RESULT 10  
 PYRK\_BACAN  
 ID PYRK\_BACAN STANDARD; PRT; 259 AA.  
 AC Q81WF3; Q6HUK1; Q6KNT6;  
 DT 14-NOV-2003, integrated into UniProtKB/Swiss-Prot.  
 DT 01-JUN-2003, sequence version 1.  
 DT 07-MAR-2006, entry version 27.  
 DE Dihydroorotate dehydrogenase electron transfer subunit.  
 GN Name=pyrK; OrderedLocusNames=BA4024, GBAA4024, BAS3736;  
 OS *Bacillus anthracis*.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC *Bacillus cereus* group.  
 OX NCBI\_TaxID=1392;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Ames / isolate Porton;  
 RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;  
 RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,  
 RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,  
 RA Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,  
 RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,  
 RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,  
 RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,  
 RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,  
 RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,  
 RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,  
 RA Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,  
 RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;  
 RT "The genome sequence of *Bacillus anthracis* Ames and comparison to  
 RT closely related bacteria.";  
 RL Nature 423:81-86(2003).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Ames ancestor;  
 RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,  
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,  
 RA Fraser C.M.;  
 RT "Bacillus anthracis comparative genomics.";  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Sterne;  
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,  
 RA Richardson P., Rubin E., Tice H.;  
 RT "Complete genome sequence of *Bacillus anthracis* Sterne.";  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.  
 CC -!- FUNCTION: Is responsible for channelling the electrons from the  
 CC oxidation of dihydroorotate from the FMN redox center in the pyrD  
 CC subunit to the ultimate electron acceptor NAD(+) (By similarity).  
 CC -!- COFACTOR: Binds 1 2Fe-2S cluster per subunit (By similarity).  
 CC -!- COFACTOR: Binds 1 FAD per subunit (By similarity).  
 CC -!- PATHWAY: Nucleotide biosynthesis; UMP biosynthesis; UMP from  
 CC HCO(3)(-): step 4.  
 CC -!- PATHWAY: Context: Pyrimidine biosynthesis.  
 CC -!- SUBUNIT: Heterotetramer of 2 pyrK and 2 pyrD subunits (By  
 CC similarity).  
 CC -!- SIMILARITY: Belongs to the pyrK family.  
 CC -----

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 CC -----  
 DR EMBL; AE016879; AAP27751.1; -; Genomic\_DNA.  
 DR EMBL; AE017334; AAT33141.1; -; Genomic\_DNA.  
 DR EMBL; AE017225; AAT56038.1; -; Genomic\_DNA.  
 DR HSSP; P56968; 1EP3.  
 DR GenomeReviews; AE016879\_GR; BA4024.  
 DR GenomeReviews; AE017225\_GR; BAS3736.  
 DR GenomeReviews; AE017334\_GR; GBAA4024.  
 DR TIGR; BA4024; -.  
 DR TIGR; GBAA4024; -.  
 DR HAMAP; MF\_01211; -; 1.  
 DR InterPro; IPR006058; 2Fe2S\_fd\_BS.  
 DR InterPro; IPR012165; Cyc3\_hyd\_g.  
 DR InterPro; IPR008333; Oxred\_FAD\_bd.  
 DR InterPro; IPR001433; Oxred\_FAD\_NAD\_bd.  
 DR InterPro; IPR000951; Ph\_dOase\_redase.  
 DR Pfam; PF00970; FAD\_binding\_6; 1.  
 DR Pfam; PF00175; NAD\_binding\_1; 1.  
 DR PIRSF; PIRSF006816; Cyc3\_hyd\_g; 1.  
 DR PRINTS; PRO0409; PHDIOXRDTASE.  
 KW 2Fe-2S; Complete proteome; Electron transport; FAD; Flavoprotein;  
 KW Iron; Iron-sulfur; Metal-binding; Pyrimidine biosynthesis; Transport.  
 FT CHAIN 1 259 Dihydroorotate dehydrogenase electron  
 FT transfer subunit.  
 FT /FTId=PRO\_0000148353.  
 FT METAL 221 221 Iron-sulfur (2Fe-2S) (By similarity).  
 FT METAL 226 226 Iron-sulfur (2Fe-2S) (By similarity).  
 FT METAL 229 229 Iron-sulfur (2Fe-2S) (By similarity).  
 FT METAL 246 246 Iron-sulfur (2Fe-2S) (By similarity).  
 SQ SEQUENCE 259 AA; 28439 MW; DC2768827E220805 CRC64;

Query Match 76.9%; Score 40; DB 1; Length 259;  
 Best Local Similarity 66.7%; Pred. No. 47;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9  
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 Db 234 QEDPSGHSY 242

RESULT 11  
 PYRK\_BACCR  
 ID PYRK\_BACCR STANDARD; PRT; 259 AA.  
 AC Q819S4;  
 DT 14-NOV-2003, integrated into UniProtKB/Swiss-Prot.  
 DT 01-JUN-2003, sequence version 1.  
 DT 07-MAR-2006, entry version 24.  
 DE Dihydroorotate dehydrogenase electron transfer subunit.  
 GN Name=pyrK; OrderedLocusNames=BC3885;  
 OS Bacillus cereus (strain ATCC 14579 / DSM 31).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 OX NCBI\_TaxID=226900;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;  
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,  
 RA Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,  
 RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,

RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,  
 RA Overbeek R., Kyrpides N.C.;  
 RT "Genome sequence of Bacillus cereus and comparative analysis with  
 RT Bacillus anthracis.";  
 RL Nature 423:87-91(2003).  
 CC -!- FUNCTION: Is responsible for channelling the electrons from the  
 CC oxidation of dihydroorotate from the FMN redox center in the pyrD  
 CC subunit to the ultimate electron acceptor NAD(+) (By similarity).  
 CC -!- COFACTOR: Binds 1 2Fe-2S cluster per subunit (By similarity).  
 CC -!- COFACTOR: Binds 1 FAD per subunit (By similarity).  
 CC -!- PATHWAY: Nucleotide biosynthesis; UMP biosynthesis; UMP from  
 CC HCO(3)(-): step 4.  
 CC -!- PATHWAY: Context: Pyrimidine biosynthesis.  
 CC -!- SUBUNIT: Heterotetramer of 2 pyrK and 2 pyrD subunits (By  
 CC similarity).  
 CC -!- SIMILARITY: Belongs to the pyrK family.  
 CC -----  
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 CC -----  
 DR EMBL; AE016877; AAP10806.1; -; Genomic\_DNA.  
 DR HSSP; P56968; 1EP3.  
 DR GenomeReviews; AE016877\_GR; BC3885.  
 DR BioCyc; BCER226900:BC3885-MONOMER; -.  
 DR HAMAP; MF\_01211; -; 1.  
 DR InterPro; IPR006058; 2Fe2S\_fd\_BS.  
 DR InterPro; IPR012165; Cyc3\_hyd\_g.  
 DR InterPro; IPR008333; Oxred\_FAD\_bd.  
 DR InterPro; IPR001433; Oxred\_FAD\_NAD\_bd.  
 DR InterPro; IPR000951; Ph\_dOase\_redase.  
 DR Pfam; PF00970; FAD\_binding\_6; 1.  
 DR Pfam; PF00175; NAD\_binding\_1; 1.  
 DR PIRSF; PIRSF006816; Cyc3\_hyd\_g; 1.  
 DR PRINTS; PR00409; PHDIOXRDTASE.  
 KW 2Fe-2S; Complete proteome; Electron transport; FAD; Flavoprotein;  
 KW Iron; Iron-sulfur; Metal-binding; Pyrimidine biosynthesis; Transport.  
 FT CHAIN 1 259 Dihydroorotate dehydrogenase electron  
 FT transfer subunit.  
 FT /FTId=PRO\_0000148354.  
 FT METAL 221 221 Iron-sulfur (2Fe-2S) (By similarity).  
 FT METAL 226 226 Iron-sulfur (2Fe-2S) (By similarity).  
 FT METAL 229 229 Iron-sulfur (2Fe-2S) (By similarity).  
 FT METAL 246 246 Iron-sulfur (2Fe-2S) (By similarity).  
 SQ SEQUENCE 259 AA; 28416 MW; D8F893A27E25919B CRC64;  
  
 Query Match 76.9%; Score 40; DB 1; Length 259;  
 Best Local Similarity 66.7%; Pred. No. 47;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 1 EADPTGHSY 9  
 : ||:||||  
 Db 234 QEDPSGHSY 242

RESULT 12  
 Q3ENC9\_BACTI  
 ID Q3ENC9\_BACTI PRELIMINARY; PRT; 259 AA.  
 AC Q3ENC9;  
 DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.  
 DT 08-NOV-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 3.

DE Dihydroorotate dehydrogenase electron transfer subunit (EC 1.3.3.1).  
GN ORFNames=RBTH\_02089;  
OS Bacillus thuringiensis serovar israelensis ATCC 35646.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
OX NCBI\_TaxID=339854;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=ATCC 35646;  
RA Anderson I., Sorokin A., Kapatral V., Reznik G., Bhattacharya A.,  
RA Mikhailova N., Burd H., Joukov V., Kaznadzey D., Walunas T.,  
RA D'Souza M., Larsen N., Pusch G., Liolios K., Grechkin Y., Lapidus A.,  
RA Goltsman E., Chu L., Fongstein M., Ehrlich D., Overbeek R.,  
RA Kyrpides N., Ivanova N.;  
RT "Comparative genome analysis of Bacillus cereus group genomes with  
RT Bacillus subtilis.";  
RL Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
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CC -----  
DR EMBL; AAJM01000353; EA052817.1; -; Genomic\_DNA.  
DR GO; GO:0004158; F:dihydroorotate oxidase activity; IEA.  
DR GO; GO:0050660; F:FAD binding; IEA.  
DR GO; GO:0005506; F:iron ion binding; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR GO; GO:0006221; P:pyrimidine nucleotide biosynthesis; IEA.  
DR InterPro; IPR012165; Cyc3\_hyd\_g.  
DR InterPro; IPR008333; Oxred\_FAD\_bd.  
DR InterPro; IPR001433; Oxred\_FAD\_NAD\_bd.  
DR InterPro; IPR000951; Ph\_dOase\_redase.  
DR Pfam; PF00970; FAD\_binding\_6; 1.  
DR Pfam; PF00175; NAD\_binding\_1; 1.  
DR PIRSF; PIRSF006816; Cyc3\_hyd\_g; 1.  
DR PRINTS; PR00409; PHDIOXRDTASE.  
KW Oxidoreductase.  
SQ SEQUENCE 259 AA; 28444 MW; E39A55E165134782 CRC64;

Query Match 76.9%; Score 40; DB 2; Length 259;  
Best Local Similarity 66.7%; Pred. No. 47;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EADPTGHSY 9  
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Db 234 QEDPSGHSY 242

RESULT 13  
Q4MJ43\_BACCE  
ID Q4MJ43\_BACCE PRELIMINARY; PRT; 259 AA.  
AC Q4MJ43;  
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.  
DT 02-AUG-2005, sequence version 1.  
DT 07-FEB-2006, entry version 2.  
DE Dihydroorotate dehydrogenase electron transfer subunit.  
GN Name=pyrDII; ORFNames=BCE\_G9241\_3870;  
OS Bacillus cereus G9241.



OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 OX NCBI\_TaxID=269801;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=G9241;  
 RX PubMed=15155910; DOI=10.1073/pnas.0402414101;  
 RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,  
 RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,  
 RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,  
 RA Rilstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,  
 RA Popovic T., Fraser C.M.;  
 RT "Identification of anthrax toxin genes in a Bacillus cereus associated  
 RT with an illness resembling inhalation anthrax."  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
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 CC -----  
 DR EMBL; AAEK01000049; EAL12213.1; -; Genomic\_DNA.  
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 DR GO; GO:0005506; F:iron ion binding; IEA.  
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 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006221; P:pyrimidine nucleotide biosynthesis; IEA.  
 DR InterPro; IPR012165; Cyc3\_hyd\_g.  
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 DR Pfam; PF00175; NAD\_binding\_1; 1.  
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 DT 25-OCT-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 11.  
 DE Dihydroorotate dehydrogenase, electron transfer subunit (EC 1.3.3.1).  
 GN Name=pyrK; OrderedLocusNames=BCE33L3644;  
 OS Bacillus cereus (strain ZK / E33L).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 OX NCBI\_TaxID=288681;  
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 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,

RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,  
 RA Richardson P., Rubin E., Tice H.;  
 RT "Complete genome sequence of *Bacillus cereus* ZK.";  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.  
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 DR EMBL; CP000001; AAU16622.1; -; Genomic\_DNA.  
 DR GO; GO:0004158; F:dihydroorotate oxidase activity; IEA.  
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 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006221; P:pyrimidine nucleotide biosynthesis; IEA.  
 DR InterPro; IPR012165; Cyc3\_hyd\_g.  
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 DR InterPro; IPR001433; Oxred\_FAD\_NAD\_bd.  
 DR InterPro; IPR000951; Ph\_dOase\_redase.  
 DR Pfam; PF00970; FAD\_binding\_6; 1.  
 DR Pfam; PF00175; NAD\_binding\_1; 1.  
 DR PIRSF; PIRSF006816; Cyc3\_hyd\_g; 1.  
 DR PRINTS; PR00409; PHDIOXRDTASE.  
 KW Complete proteome; Oxidoreductase.  
 SQ SEQUENCE 259 AA; 28439 MW; DC2768827E220805 CRC64;

Query Match 76.9%; Score 40; DB 2; Length 259;  
 Best Local Similarity 66.7%; Pred. No. 47;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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 RA Richardson P., Rubin E., Tice H.;  
 RT "Complete genome sequence of *Bacillus thuringiensis* 97-27.";  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.  
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 DR EMBL; AE017355; AAT60634.1; -; Genomic\_DNA.

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 KW Complete proteome; Oxidoreductase.  
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 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EADPTGHSY 9  
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Search completed: August 25, 2006, 00:59:28  
 Job time : 302 secs

SCORE 1.3 BuildDate: 12/06/2005

# SCORE Search Results Details for Application 08819669 and Search Result us-08-819-669e- 8.rge.

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OM nucleic - nucleic search, using sw model

Run on: August 25, 2006, 09:08:38 ; Search time 30844 Seconds  
(without alignments)  
11763.639 Million cell updates/sec

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Perfect score: 5674  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_pat:\*  
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4: gb\_pl:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_sts:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vi:\*  
11: gb\_ov:\*  
12: gb\_htg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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	2	5674	100.0	5674	2	AR153499	AR153499 Sequence
	3	5674	100.0	5674	2	I24013	I24013 Sequence 1
	4	5674	100.0	5674	2	I36923	I36923 Sequence 8
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	6	5674	100.0	5674	2	AR322041	AR322041 Sequence
	7	5674	100.0	5674	2	AR361125	AR361125 Sequence
	8	5674	100.0	5674	2	AR721150	AR721150 Sequence
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	15	2654.8	46.8	161664	5	U82696	U82696 Homo sapien
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c	43	2353	41.5	168595	12	AC146354	AC146354 Macaca mu
	44	2328	41.0	178515	12	AC009621	AC009621 Homo sapi
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# ALIGNMENTS

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AR060975

LOCUS AR060975 5674 bp DNA linear PAT 29-SEP-1999  
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 ACCESSION AR060975  
 VERSION AR060975.1 GI:5988666  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 5674)  
 AUTHORS Chen,Y.-T., Stockert,E., Chen,Y., Garin-Chesa,P., Rettig,W.J. and Old,L.J.  
 TITLE Tumor rejection antigen precursor  
 JOURNAL Patent: US 5843448-A 1 01-DEC-1998;  
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 /organism="unknown"  
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Query Match 100.0%; Score 5674; DB 2; Length 5674;  
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Qy    121 CTCTCAACCCAGGGAAGCCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
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Qy    181 TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
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Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

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Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480
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Qy	1381	GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
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Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCATTTAATGGTTCTGAGGGGCGGCTTGAG	1500
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Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACTCTTGATTGGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACTCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360

Db	3301	 CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCTCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACCTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACCTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260

Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTCAATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTCAATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCCAAGACAGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCCAAGACAGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
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Qy	4561	GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
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Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160

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Qy      5161 AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA 5220
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Db      5161 AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA 5220

Qy      5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA 5280
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Db      5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA 5280

Qy      5281 ATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT 5340
        |||
Db      5281 ATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT 5340

Qy      5341 TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400
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Db      5341 TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400

Qy      5401 TCTGCTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAAC 5460
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Db      5401 TCTGCTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAAC 5460

Qy      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
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Db      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520

Qy      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTTGGGGCTCCGGGTGAGAGTG 5580
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Db      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTTGGGGCTCCGGGTGAGAGTG 5580

Qy      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT 5640
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Db      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT 5640

Qy      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
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Db      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

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# RESULT 2

AR153499

LOCUS AR153499 5674 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 8 from patent US 6235525.

ACCESSION AR153499

VERSION AR153499.1 GI:15121031

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 5674)

AUTHORS van den Eynde,B., van der Bruggen,P. and Boon-Falleur,T.

TITLE Isolated nucleic acid molecules coding for tumor rejection antigen precursor MAGE-3 and uses thereof

JOURNAL Patent: US 6235525-A 8 22-MAY-2001;

FEATURES Location/Qualifiers

source 1. .5674

/organism="unknown"

/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 5674; DB 2; Length 5674;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CCCCGGGACCACTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC	60
Db	1	CCCCGGGACCACTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC	60
Qy	61	ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG	120
Db	61	ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG	120
Qy	121	CTCTCAACCCAGGGAAGCCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG	180
Db	121	CTCTCAACCCAGGGAAGCCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG	180
Qy	181	TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Db	181	TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Qy	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Db	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Qy	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Db	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Qy	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Db	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Qy	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Db	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Qy	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Db	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Qy	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCCCTTTCATTGTCATTCCAACCCCCA	600
Db	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCCCTTTCATTGTCATTCCAACCCCCA	600
Qy	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCATCCGCCAGCCATTCACCCCT	660
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Qy	661	CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Db	661	CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Qy	721	CCAGGAAACATCCGGGTGCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721	CCAGGAAACATCCGGGTGCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900

Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAATGATCCAGTACCACCCCTGCTG	1620
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Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800

Qy	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCACATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCACATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGGCTCAGAGGACCCAGCACCTTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGGCTCAGAGGACCCAGCACCTTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
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Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
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Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
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Db	2701	TCACCCAGGATGTGGCTTCTTTTTCCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
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Qy	2881	GACCAGAACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCAGAG	2940
Db	2881	GACCAGAACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCAGAG	2940
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Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
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Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
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Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
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Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
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Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
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Db	3601	TCAGTCCTGTAGAAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
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Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
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Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
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Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
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Qy	4261	AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
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Qy	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCCACCGGCCA	4380
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Qy	4381	CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCTTGCTGGGTGATAATCA	4440
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Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560

Qy	4561	GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
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Qy	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
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Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
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Qy	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAC	5460
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Qy      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
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Qy      5521 CTCCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
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Db      5521 CTCCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580

Qy      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTCTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
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Qy      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
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# RESULT 3

I24013

LOCUS I24013 5674 bp DNA linear PAT 07-OCT-1996

DEFINITION Sequence 1 from patent US 5541104.

ACCESSION I24013

VERSION I24013.1 GI:1603883

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 5674)

AUTHORS Chen,Y.-T., Stockert,E., Chen,Y., Garin-Chesa,P., Rettig,W.J., van der Bruggen,P., Boon-Falleur,T. and Old,L.J.

TITLE Monoclonal antibodies which bind to tumor rejection antigen precursor mage-1

JOURNAL Patent: US 5541104-A 1 30-JUL-1996;

FEATURES Location/Qualifiers

source 1. .5674

/organism="unknown"

/mol\_type="unassigned DNA"

## ORIGIN

Query Match 100.0%; Score 5674; DB 2; Length 5674;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy      61 ATCCAAACATCTTCACGCTCACCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
        |||
Db      61 ATCCAAACATCTTCACGCTCACCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy      121 CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
        |||
Db      121 CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy      181 TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
        |||
Db      181 TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy      241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
        |||

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Db	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Qy	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Db	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Qy	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Db	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Qy	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Db	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Qy	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Db	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Qy	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Db	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Qy	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT	660
Db	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT	660
Qy	661	CACCCCCACCCCCACCCCCACGCCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Db	661	CACCCCCACCCCCACCCCCACGCCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Qy	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
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Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC	1200

Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
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Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTAGGACACCGCACCCCTGTCTGAG	2100

Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTTCCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
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Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTCAGCCCTGGACACC	2700
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Qy	2761	CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
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Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCCAGAG	2940
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Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCTGGGATCATTGATGTCAGGG	3000
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Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060

Db	3001	 ACGGGGAGGCCCTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	 CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	 GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Db	3181	 GTCCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
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Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	 CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCT	3420
Db	3361	 GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	 CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAA	3540
Db	3481	 ACAGAGCAGAGGATGCACAGGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	 GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
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Db	3601	 TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	 CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Db	3721	 GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781	 AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	 CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCTGGTGTG	3960

Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCCTCCTCCTGCTGCTGGGCACCCCTGGAGGAGGTGCC	4020
Db	3961		4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021		4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081		4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCATAAGAAGGTGGC	4200
Db	4141		4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201		4260
Qy	4261	AATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGC	4320
Db	4261		4320
Qy	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321		4380
Qy	4381	CTCCTATGTCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381		4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCTGGTTCATGATTGCAATGGAGGGCGG	4500
Db	4441		4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501		4560
Qy	4561	GGAGCACAGTGCCATGTTGGGAGCCAGGAAGCTGCTCACCAGATTTGGTGCAGGAAAA	4620
Db	4561		4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621		4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681		4740
Qy	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
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Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCTTCACTCT	4920
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Qy	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
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Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCATTTTGTGAATTGGGATAAT	5160
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Qy	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATA	5460
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Qy	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Db	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Qy	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCT	5640
Db	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCT	5640
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RESULT 4

I36923

LOCUS

I36923

5674 bp

DNA

linear

PAT 13-MAY-1997

DEFINITION Sequence 8 from patent US 5612201.  
 ACCESSION I36923  
 VERSION I36923.1 GI:2084883  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 5674)  
 AUTHORS De Plaen,E., Boon-Falleur,T., Lethe,B., Szikora,J.-P., De Smet,C.  
 and Chomez,P.  
 TITLE Isolated nucleic acid molecules useful in determining expression of  
 a tumor rejection antigen precursor  
 JOURNAL Patent: US 5612201-A 8 18-MAR-1997;  
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 ORIGIN

Query Match 100.0%; Score 5674; DB 2; Length 5674;  
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Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
      |||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
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Db    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
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Db    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
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Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
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Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
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Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480
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Qy    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540
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Qy    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600
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Db	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Qy	661	CACCCCCACCCCCACCCCCACGCCCCTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Db	661	CACCCCCACCCCCACCCCCACGCCCCTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Qy	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
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Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
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Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGAAGA	960
Db	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
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Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC	1200
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Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
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Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500

Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGTCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
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Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
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Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTGAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTGAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
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Qy	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
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Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
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Db	3001	ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
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Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
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Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
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Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
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Qy	3781		AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781		AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841		CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
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Qy	4081		CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081		CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141		GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141		GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201		TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260

Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTCAATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
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Qy	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
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Qy	4381	CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCATATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCATATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
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Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
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Qy	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
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Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
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Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
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Qy      5161 AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA 5220
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Qy      5341 TAAATCTGAATAAAGAATTCTTCTGTTCAGTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400
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Db      5341 TAAATCTGAATAAAGAATTCTTCTGTTCAGTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400

Qy      5401 TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5401 TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460

Qy      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520

Qy      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580

Qy      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640

Qy      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
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Db      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

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RESULT 5

AR268060

LOCUS AR268060 5674 bp DNA linear PAT 10-APR-2003

DEFINITION Sequence 8 from patent US 6498021.

ACCESSION AR268060

VERSION AR268060.1 GI:29698299

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 5674)

AUTHORS Guagler,B.

TITLE Isolated nucleic acid molecules coding for tumor rejection antigen precursor MAGE-8 and uses thereof

JOURNAL Patent: US 6498021-A 8 24-DEC-2002;  
Ludwig Institute for Cancer Research; New York, NY

FEATURES Location/Qualifiers

source 1..5674

/organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 5674; DB 2; Length 5674;



Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
      |||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
      |||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
      |||
Db    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
      |||
Db    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
      |||
Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
      |||
Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
      |||
Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480
      |||
Db    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

Qy    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540
      |||
Db    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540

Qy    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600
      |||
Db    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600

Qy    601 CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT 660
      |||
Db    601 CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT 660

Qy    661 CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG 720
      |||
Db    661 CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG 720

Qy    721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780
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Db    721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780

Qy    781 GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840
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Db    781 GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840

Qy    841 CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA 900
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Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800

Qy	1801	ACCCTGGGAGGGAAGTGAAGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAAGTGAAGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAGGGGTCAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAGGGGTCAGCCCTGGACACC	2700

Qy	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGAAGTCAAGTACAGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGAAGTCAAGTACAGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGCTCTGCCGAGGTCCTTCGTTATCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGCTCTGCCGAGGTCCTTCGTTATCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660

Db	3601	TCAGTCCTGTAGAAATCGACCTCTGCTGGCCGGCTGTACCCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCTTTGTACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCTTTGTACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560

Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCAAGATTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCAAGATTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCGTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCGTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGGAAATGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGGAAATGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Db	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAC	5460

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Qy      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
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Db      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520

Qy      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
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Db      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580

Qy      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
        |||
Db      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640

Qy      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
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Db      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

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# RESULT 6

AR322041

LOCUS AR322041 5674 bp DNA linear PAT 17-AUG-2003

DEFINITION Sequence 8 from patent US 6565857.

ACCESSION AR322041

VERSION AR322041.1 GI:33707547

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 5674)

AUTHORS van den Eynde,B., van den Bruggen,P. and Boon-Falleur,T.

TITLE Methods for treating a disorder by using Mage-3 or Mage-3 related materials

JOURNAL Patent: US 6565857-A 8 20-MAY-2003;

Ludwig Institute for Cancer Research; New York, NY

FEATURES Location/Qualifiers

source 1. .5674

/organism="unknown"

/mol\_type="genomic DNA"

## ORIGIN

Query Match 100.0%; Score 5674; DB 2; Length 5674;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
        |||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy      61 ATCCAAACATCTTCACGCTCACCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
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Db      61 ATCCAAACATCTTCACGCTCACCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

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Db      121 CTCTCAACCCAGGGAAGCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy      181 TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
        |||
Db      181 TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy      241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

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Db	241		300
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Qy	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
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Qy	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
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Db	481		540
Qy	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Db	541		600
Qy	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT	660
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Qy	661	CACCCCCACCCCAACCCCAACGCCACTCCACCCCAACCCAGGCAGGATCCGGTTCCCG	720
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Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
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Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
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Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901		960
Qy	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
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Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021		1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081		1140
Qy	1141	CCAAGACTGCCTCCAATCCCCACTCCACCCCATTCGCATTCCCATCCCCACCCAACC	1200



Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTAGGACACCGCACCCCTGTCTGAG	2100

Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTGAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTGAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000

Qy	3001	ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCTGGTGTG	3960

Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
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Db	3961	TGTGCAGGCTGCCACCTCCTCCTCCTCCTCCTGCTGCTGGGCACCTGGAGGAGGTGCC	4020
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Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACCTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACCTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
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Qy	4561	GGAGCACAGTGCCATGGGGAGCCCAGGAAGCTGCTCACCAAGATTTGGTGCAGGAAAA	4620
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Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
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Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGACTGGGCCAGTGCACCTT	4860

Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
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Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
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Qy	5101	TAAGAGTCTTGTTGTTTTATTTCAGATTGGGAAATCCATTCTATTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTTGTTTTATTTCAGATTGGGAAATCCATTCTATTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
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Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
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Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
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Qy	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
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Qy	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
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Qy	5521	CTCTAAAGATGTAGGGAAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Db	5521	CTCTAAAGATGTAGGGAAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Qy	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT	5640
Db	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT	5640
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RESULT 7  
AR361125

LOCUS AR361125 5674 bp DNA linear PAT 17-AUG-2003  
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 VERSION AR361125.1 GI:33768828  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 5674)  
 AUTHORS Guagler,B., Van den Eynde,B., van den Bruggen,P. and  
 Boon-Falleur,T.  
 TITLE Methods for diagnosing a disorder by assaying for MAGE-3  
 JOURNAL Patent: US 6599699-A 8 29-JUL-2003;  
 Ludwig Institute for Cancer Research; New York, NY  
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ORIGIN

Query Match 100.0%; Score 5674; DB 2; Length 5674;  
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Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
      |||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
      |||
Db    121 CTCTCAACCCAGGGAAGCCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
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Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
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Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
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Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
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Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480
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Qy    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540
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Qy	661		CACCCCCACCCCAACCCCAACGCCCCTCCACCCCAACCCAGGCAGGATCCGGTTCCCG	720
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Qy	721		CCAGGAAACATCCGGGTGCCCCGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
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Qy	901		GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGAAGA	960
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Db	961		CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021		TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021		TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081		GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081		GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141		CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141		CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201		CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Db	1201		CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Qy	1261		ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCCTCACTGCCCCAAC	1320
Db	1261		ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCCTCACTGCCCCAAC	1320
Qy	1321		CCCACCCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAAATCC	1380
Db	1321		CCCACCCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAAATCC	1380
Qy	1381		GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381		GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441		TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500

Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTCAATTTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAAGTGAAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAAGTGAAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400



Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACC AAAGGGGTCAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACC AAAGGGGTCAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGCTGCGGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGCTGCGGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCC TTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCC TTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAAC TCTTGATTGGATTCTCAG	3240
Db	3181	GTCCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAAC TCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300

Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTTCCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTTCCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCGTAGAAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCGTAGAAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
Db	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCCTCCTCCTGCTGCTGGGCACCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCCTCCTCCTGCTGCTGGGCACCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260

Db	4201	 TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGC	4320
Db	4261	 AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	 CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTGATAATCA	4440
Db	4381	 CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	 GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	 CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTGGGTGCAGGAAAA	4620
Db	4561	 GGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTGGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Db	4621	 GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	 CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	 GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	 GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
Db	4861	 CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	 GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	 TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Db	5041	 TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160

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Db      5101 TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT 5160
Qy      5161 AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA 5220
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Db      5161 AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA 5220
Qy      5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA 5280
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Db      5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA 5280
Qy      5281 ATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT 5340
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Db      5281 ATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT 5340
Qy      5341 TAAATCTGAATAAAGAATTCTTCTGTTCACCTGGCTCTTTTCTTCTCCATGCAGTGCAGCA 5400
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Db      5341 TAAATCTGAATAAAGAATTCTTCTGTTCACCTGGCTCTTTTCTTCTCCATGCAGTGCAGCA 5400
Qy      5401 TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAAC 5460
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Db      5401 TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAAC 5460
Qy      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
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Db      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Qy      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
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Db      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Qy      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
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Db      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
Qy      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
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Db      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

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# RESULT 8

AR721150

LOCUS AR721150 5674 bp DNA linear PAT 07-OCT-2005

DEFINITION Sequence 8 from patent US 6946289.

ACCESSION AR721150

VERSION AR721150.1 GI:77372626

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 5674)

AUTHORS Guagler,B., van den Eynde,B., van der Bruggen,P. and Boon-Falleur,T.

TITLE Isolated nucleic acid molecules coding for tumor rejection antigen precursor Mage-6 and uses thereof

JOURNAL Patent: US 6946289-A 8 20-SEP-2005;

Ludwig Institute for Cancer Research; New York, NY

FEATURES Location/Qualifiers

source 1. .5674

/organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 5674; DB 2; Length 5674;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
        |||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCACCCCTG 120
        |||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
        |||
Db    121 CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
        |||
Db    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
        |||
Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
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Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
        |||
Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCCTGCCAGACAT 480
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Db    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCCTGCCAGACAT 480

Qy    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540
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Db    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540

Qy    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600
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Qy    601 CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT 660
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Qy    661 CACCCCCACCCCAACCCACGCCCCTCCACCCCAACCCAGGCAGGATCCGGTTCCTCG 720
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Db    661 CACCCCCACCCCAACCCACGCCCCTCCACCCCAACCCAGGCAGGATCCGGTTCCTCG 720

Qy    721 CCAGGAAACATCCGGGTGCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780
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Db    721 CCAGGAAACATCCGGGTGCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780

Qy    781 GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840
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Db    781 GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840
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Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGCCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGCCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCCGCATTAGGGTCAGG	1800

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Db	2461	 TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTAACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
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Db	2581	 ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
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Db	2881	GACCAGAACACTGAGGGAGACTGC	CACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCG	AGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCG	AGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
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Qy	3181	GTCCCCTCCTGTCCTTCCATT	CCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
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Db	3481	ACAGAGCAGAGGATGCACAG	GGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
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Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
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Qy	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
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# RESULT 9

AC152005/c

LOCUS AC152005 88597 bp DNA linear PRI 20-OCT-2004

DEFINITION Homo sapiens chromosome X clone CTC-233o10 map q28, complete sequence.

ACCESSION AC152005

VERSION AC152005.1 GI:54306089

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 88597)

AUTHORS Mallon,A.M., Platzner,M., Bate,R., Gloeckner,G., Botcherby,M.R., Nordsiek,G., Strivens,M.A., Kioschis,P., Dangel,A., Cunningham,D., Straw,R.N., Weston,P., Gilbert,M., Fernando,S., Goodall,K., Hunter,G., Greystrom,J.S., Clarke,D., Kimberley,C., Goerdes,M., Blechschmidt,K., Rump,A., Hinzmann,B., Mundy,C.R., Miller,W., Poustka,A., Herman,G.E., Rhodes,M., Denny,P., Rosenthal,A. and Brown,S.D.

TITLE Comparative genome sequence analysis of the Bpa/Str region in mouse and Man

JOURNAL Genome Res. 10 (6), 758-775 (2000)

PUBMED 10854409

REFERENCE 2 (bases 1 to 88597)

AUTHORS Lagemann,D. and Platzner,M.

TITLE Direct Submission

JOURNAL Submitted (20-OCT-2004) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany

COMMENT ----- Genome Center

Center: Institute of Molecular Biotechnology

Center code: IMB

Web site: <http://genome.imb-jena.de/>

Contact: [gscj-submit@genome.imb-jena.de](mailto:gscj-submit@genome.imb-jena.de)

----- Project Information

Center project name: 233o

Center clone name: CTC-233o10

----- Summary Statistics

Sequencing vector: M13mpl8; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329  
Consensus quality: 88596 bases at least Q40  
Consensus quality: 88597 bases at least Q30  
Consensus quality: 88597 bases at least Q20  
Quality coverage: 21.98x

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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

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Neighboring sequence information:  
This clone is overlapped by RP11-76K17, G248-85942H2, G248-86799C8, Qc-15B1, Qc-3H10, Qc-13B12.

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Sequence Quality Assessment:  
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.  
All manually edited bases have been reduced to quality zero.  
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.  
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

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ORIGIN

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Matches 5655;  Conservative 0;  Mismatches 17;  Indels 7;  Gaps 7;

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Qy	1140	CCCAAGACTGCACTCCAATCCCCACTCCACCCCATTCGCATTCCCATTCCCCACCCAAC	1199
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Qy	1200	CCCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCAC	1259
Db	57374	CCCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCAC	57315
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Db	57314	CACCTTCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAA	57255
Qy	1320	CCCCACCCTCATCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATCTGGCAGAATC	1379
Db	57254	CCCCACCCTCATCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATCTGGCAGAATC	57195
Qy	1380	CGGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGAC	1439
Db	57194	CGGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGATGGCCCGATGTGAAACCACTGAC	57135
Qy	1440	TTGAACCTCACAGATCTGAGAGAAGCCAGGTTCAATTAATGGTTCTGAGGGGCGGCTTGA	1499
Db	57134	TTGAACCTCACAGATCTGAGAGAAGCCAGGTTCAATTAATGGTTCTGAGGGGCGGCTTGA	57075
Qy	1500	GATCCACTGAGGGGAGTGGTTTATAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAG	1559

Db	57074	 GATCCACTGAGGGGAGTGGTTTATAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAG	57015
Qy	1560	GACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCT	1619
Db	57014	 GACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCT	56955
Qy	1620	GCCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTC	1679
Db	56954	 GCCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTC	56895
Qy	1680	CCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGT	1739
Db	56894	 CCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGT	56835
Qy	1740	TGGTCAGGAGA-GGCAGGGCCCAGGCATCAAGGTCCA-GCATCCGCCCGGCATTAGGGTC	1797
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Qy	1798	AGGACCCTGGGAGGGAAGTGGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCC	1857
Db	56774	 AGGACCCTGGGAGGGAAGTGGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCC	56715
Qy	1858	ACCCCACTCACATTCCCATACTACCCCTACCCCAACCTCATCTTGTCAGAATCCCTG	1917
Db	56714	 ACCCCACTCACATTCCCATACTACCCCTACCCCAACCTCATCTTGTCAGAATCCCTG	56655
Qy	1918	CTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCAT	1977
Db	56654	 CTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCAT	56595
Qy	1978	CCAGGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCC	2037
Db	56594	 CCAGGG-CTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCC	56536
Qy	2038	TACTGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTAGGACACCGCACCCCTGTCT	2097
Db	56535	 TACTGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTAGGACACCGCACCCCTGTCT	56476
Qy	2098	GAGACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATT-GCAT	2156
Db	56475	 GAGACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTAGCAT	56416
Qy	2157	GGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGA	2216
Db	56415	 GGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGA	56356
Qy	2217	CCTTGGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGCCACA	2276
Db	56355	 CCTTGGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGCCACA	56296
Qy	2277	TATGGCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGG	2336
Db	56295	 TATGGCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGG	56236
Qy	2337	GGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTT	2396
Db	56235	 GGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTT	56176
Qy	2397	CATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCC	2456

Db	56175	CATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCC	56116
Qy	2457	CCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGT	2516
Db	56115	CCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGT	56056
Qy	2517	ACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGAT	2576
Db	56055	ACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGAT	55996
Qy	2577	GTCTACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGAT	2636
Db	55995	GTCTACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGAT	55936
Qy	2637	GAGTGAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTCAGCCCTGGA	2696
Db	55935	GAGTGAGACAGACAAGGCTATTGGAATCCTCACCCCAGAACCAGGGGTCAGCCCTGGA	55876
Qy	2697	CACCTCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGG	2756
Db	55875	CACCTCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGG	55817
Qy	2757	ACCTCATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAG	2816
Db	55816	ACCTCATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAG	55757
Qy	2817	AGCGGTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACC	2876
Db	55756	AGCGGTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACC	55697
Qy	2877	CCAGGACCAGAACACTGAGGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCC	2936
Db	55696	CCAGGACCAGAACACTGAGGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCC	55637
Qy	2937	AGAGAGCATGGGCTGGGCCGCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTC	2996
Db	55636	AGAGAGCATGGGCTGGGCCGCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTC	55577
Qy	2997	AGGGACGGGGAGGCC TTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCA	3056
Db	55576	AGGGACGGGGAGGCC TTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCA	55517
Qy	3057	GGCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTC	3116
Db	55516	GGCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTC	55457
Qy	3117	CAATGAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGAT	3176
Db	55456	CAATGAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGAT	55397
Qy	3177	GTTTGTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAAC TCTTGATT TGGATTTC	3236
Db	55396	GTTTGTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAAC TCTTGATT TGGATTTC	55337
Qy	3237	TCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTG	3296
Db	55336	TCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTG	55277
Qy	3297	AGAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCT	3356
Db	55276	AGAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCT	55217



Qy	3357	CCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGAT	3416
Db	55216	CCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGAT	55157
Qy	3417	TCCTCTTCCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCA	3476
Db	55156	TCCTCTTCCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCA	55097
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Db	54976	ACTGTCAGTCCGTGTAGAATCGACCTCTGCTGGCCGGCTGTACCTGAGTACCTCTCACT	54917
Qy	3657	TCCTCCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCAC	3716
Db	54916	TCCTCCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCAC	54857
Qy	3717	AGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGT	3776
Db	54856	AGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGT	54797
Qy	3777	TCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCC	3836
Db	54796	TCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCC	54737
Qy	3837	AGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGA	3896
Db	54736	AGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGA	54677
Qy	3897	GGAGTCTGCAC TGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG	3956
Db	54676	GGAGTCTGCAC TGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG	54617
Qy	3957	TGTGTGTGCAGGCTGCCACCTCCTCCTCCTCCTCCTGCTCCTGGGCACCTGGAGGAGG	4016
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Qy	4017	TGCCCAC TGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCA	4076
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Qy	4077	CTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGG	4136
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Qy	4137	AGGGGCCAAGCACCTCTTGATCCTGGAGTCTTGTTCCGAGCAGTAATCACTAAGAAGG	4196
Db	54436	AGGGGCCAAGCACCTCTTGATCCTGGAGTCTTGTTCCGAGCAGTAATCACTAAGAAGG	54377
Qy	4197	TGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGG	4256
Db	54376	TGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGG	54317

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Qy 4317 AAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCG 4376  
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Qy 4377 GCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATA 4436  
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Qy 4557 GGAGGGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGG 4616  
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 Db 54016 GGAGGGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGG 53957

Qy 4617 AAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGT 4675  
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Qy 4916 ACTCTGAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGG 4975  
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 Db 53656 ACTCTGAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGG 53597

Qy 4976 AGATTTATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAA 5035  
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 Db 53596 AGATTTATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAA 53537

Qy 5036 TGAACCTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTT 5095  
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Qy 5156 ATAATAACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGA 5215

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Qy      5216 GATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCT 5275
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Qy      5276 GTAAAATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGA 5335
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Qy      5336 GAAATTAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACT 5395
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Qy      5396 GAGCATCTGCTTTTGGGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACT 5455
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Qy      5456 CATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAG 5515
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Qy      5516 ATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGA 5575
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Qy      5576 GAGTGGTGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTC 5635
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Qy      5636 CTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
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Db      52936 CTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 52898

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# RESULT 10

AC153070/c

LOCUS AC153070 40359 bp DNA linear PRI 01-DEC-2004

DEFINITION Homo sapiens chromosome X clone Qc-15B1 map q28, complete sequence.

ACCESSION AC153070

VERSION AC153070.1 GI:56158998

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 40359)

AUTHORS Platzer,M., Michaelis,E. and Heinze,I.

TITLE Chromosome X genomic sequence

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 40359)

AUTHORS Lagemann,D. and Platzer,M.

TITLE Direct Submission

JOURNAL Submitted (01-DEC-2004) Genome Analysis, Institute of Molecular  
Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany

COMMENT ----- Genome Center

Center: Institute of Molecular Biotechnology

Center code: IMB

Web site: <http://genome.imb-jena.de/>

Contact: gscj-submit@genome.imb-jena.de

----- Project Information

Center project name: X65

Center clone name: Qc-15B1

----- Summary Statistics

Sequencing vector: M13mpl8; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 40359 bases at least Q40

Consensus quality: 40359 bases at least Q30

Consensus quality: 40359 bases at least Q20

Quality coverage: 20.90x

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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

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Neighboring sequence information:

This clone is overlapped by CTC-233o10, Qc-3H10, Qc-13B12.

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Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

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FEATURES	Location/Qualifiers
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source	1. .39172 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="CTC-233o10" /note="overlapping clone"
source	13557. .40359 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="Qc-3H10" /note="overlapping clone"
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ORIGIN

Query Match 97.6%; Score 5535.8; DB 5; Length 40359;  
 Best Local Similarity 99.3%; Pred. No. 0;  
 Matches 5642; Conservative 0; Mismatches 27; Indels 10; Gaps 8;

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Db	9070	CCCGGGGCACCACTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC	9011
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Qy	121	CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG	180
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Qy	181	TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
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Qy	241	CCCA-GCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCC	299
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Qy	300	CAGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTT	359
Db	8770	CAGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTT	8711
Qy	360	CTCAGGCTGGGCCACCCCGACCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGA	419
Db	8710	CTCAGGCTGGGCCACCCCGACCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAG	8651
Qy	420	GCTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACA	479
Db	8650	AGCTCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACA	8591
Qy	480	TCATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAA	539
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Qy	540	CCCCCACTCCAATGCTCACTCCCGTGACCAACCCCTCTTCATTGTCATTCCAACCCCC	599
Db	8530	CCCCCACTCCAATGCTCACTCCCGTGACCAACCCCTCTTCATTGTCATTCCAACCCCC	8471
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Qy	720	GCCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAG	779
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Qy	780	AGAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAG	839
Db	8290	AGAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAG	8231

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Qy	900	AGAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCCACCCGCGGAAG	959
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Db	8110	ACGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTT	8051
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Qy	1080	GGCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCC	1139
Db	7990	GGCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCC	7931
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Qy	1200	CCCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCAC	1259
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Db	7690	CGGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGATGGCCCGATGTGAAACCACTGAC	7631
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Db	7570	GATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAG	7511
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Db	7510	GACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCT	7451
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Qy	3177	GTTTGTCCCCCTCCTGTCTTCCATTTCCTTATCATGGATGTGAACCTCTTGATTGATTTC	3236
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RESULT 11

AC116666/c

LOCUS AC116666 169351 bp DNA linear PRI 06-FEB-2003

DEFINITION Homo sapiens chromosome X clone RP11-329E24 map q28, complete sequence.

ACCESSION AC116666 AC024727 AF134576

VERSION AC116666.2 GI:28261468

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 169351)

AUTHORS Galgoczy, P., Wen, G. and Platzter, M.

TITLE Chromosome X genomic sequence

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 169351)

AUTHORS Platzter, M.

TITLE Direct Submission

JOURNAL Submitted (02-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany

REFERENCE 3 (bases 1 to 169351)

AUTHORS Platzter, M.

TITLE Direct Submission

JOURNAL Submitted (06-FEB-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany

COMMENT On or before Feb 6, 2003 this sequence version replaced gi:13786263, gi:19881535.

----- Genome Center

Drafting Center: Washington Univ. Genome Sequencing Center

Finishing Center: Institute of Molecular Biotechnology

Center code: IMB

Web site: <http://genome.imb-jena.de/>

Contact: [gscj-submit@genome.imb-jena.de](mailto:gscj-submit@genome.imb-jena.de)

----- Project Information

Center project name: X164

Center clone name: RP11-329E24

----- Summary Statistics

Sequencing vector: M13, pUC18; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329  
Consensus quality: 169243 bases at least Q40  
Consensus quality: 169295 bases at least Q30  
Consensus quality: 169351 bases at least Q20  
Quality coverage: 16.11x

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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.  
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This clone was finished using overlapping sequence from accession AC009621 drafted by WIBR.  
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Neighboring sequence information:

This entry is overlapped by RP1-73F14, RP11-1007I13, RP11-157E12 and covers Qc-3H5, ICRFXc104-3G5, Qc-16C3, Qc-4H4 entirely.  
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Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.  
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Qy      180 GTTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGG 239
      || || || || || || || || || || || || || || || || || || || || ||
Db      53720 GTCAAAGAGAAGCGAAGTTCTCGCTCTGAGTGGCGGCTTGAGATTGGTGGAGGGAAGTGG 53661

Qy      240 GCCCA-GCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACC 298

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Db	53660	GTCCAGGCTCTGTGAAGAGGCAAGGTGAGACTCTAAGGGAGGACTCAGGAGGCCCCACC	53601
Qy	299	CCAGATAGAGGACCCCAAATAATCC-----CTTCATGCCAGTCTCTGGACCATCTGG	349
Db	53600	CCAGATAGAGGGCCCCAAATAATCCAGCACTACTCTGCTGCCAGCCCTAAACCACCTGG	53541
Qy	350	TGGTGGACTTCTCAGGCTGGGGCACCCCCAGCCCCCT-----TGCTGCTTAAACCA	400
Db	53540	GGGCGGACTTCTCAGTCTGGGGCACTCCCTGCACCTGCCAGCCCTGTGGCTTAAACCG	53481
Qy	401	CTGGGGACTC-GAAGTCAGAGCTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAG	459
Db	53480	CAAGGGACTCTGGAGTCAGAGCTTCGTGTGACCAAGGCAGGGCTGGTTAGGAGAGGGCAG	53421
Qy	460	CGTCCAGGCTCTGCCAGACATCATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAG	519
Db	53420	TGGCCAAGCTCTGCCAGGCATCAACATCAGGACCCTAAGTGAGGGCTGAGGGCCCCAAC	53361
Qy	520	ACCC---CACTCCCGTGACCCAAACCCCACTCCAATGCTCACTCCCGTGACCCAACCCCC	576
Db	53360	CCCCATTCCCATCCCCACCCCATCCCATTTCCATCCCCATCCCCACCTCCATCCCCCA	53301
Qy	577	TCTTCATTGTCAATCCAACCCCCACCCACATCCCCACCCCATCCCTCAACCTGATGC	636
Db	53300	CCAGAACCCCTATCCCCACCAGAAACCCTATCCTGCCCACTCCCCACCACGTTTCATCCC	53241
Qy	637	CCATCCGCCCCA-GCCATTCCACCCTCACCCCCACCCCAACCCCAAGGCTGACCCCTCC	695
Db	53240	TACTCCCACCATTCCCATCTTCCCCACCCCTGACCTCCTCCTCACCTCCCACCCCCC	53181
Qy	696	CCACCCAGGCAGGATCCGG-----TTCCCGCCAGGAAACATCCGGGTGCCCG	742
Db	53180	ACACCCTGGCAGAATTTCGGTTCTGCTCCTGCTTTCAACCCAGGGAATCCCTGGGTGACCA	53121
Qy	743	GATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGAGAAGCGAGGTTTCCATTCTGAG	802
Db	53120	GATGTGGTGCCACTGTCTTGACATTTGAGGTCGGAGAGAAGCAAGGGCCTCGCTCTCAG	53061
Qy	803	GGACGGCGTAGAGTTTCGGCCGAAGGAACCTGACCCAGGCTCTGTGAGGAGGCAAGGTGAG	862
Db	53060	GGGCAGC-TGGAGATCAGCTGAGGGCAGCTGGCCCTGGCTCTGTGAGGATGCAAGGTGAG	53002
Qy	863	AGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAATAGAGAGCCCCAAATATTCCAG--	920
Db	53001	ATGCTGAGGGAGGACTAAGGAGTATCCACCCCTGGTAGTGGACCCCAAATAATCCAGTG	52942
Qy	921	-CCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGACGTCTCAGCCTGGGCTGCC	979
Db	52941	CCACCTCTCCTGCTGCTAGCTCTGGACCATCCAGGGCAGGACTCCTTAGGCTGGGCCACC	52882
Qy	980	CCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTCTTCTCCCCAAGCTCTGGAA	1039
Db	52881	CCCAGTCCCCCACCCTTAAGCCGCAGGGGA-----CTCAGGAG	52843
Qy	1040	TCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGGGCAGGGCACAGGCTCTGCC	1099
Db	52842	ACAGAGCTTGGTATGACCAGGGCAGGACTGGTTAGGAGAGGACAGCTCCCAGGCTCTGCC	52783
Qy	1100	AGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCCCCAAGACTGCACTCCAATC	1159

Db 52782 AGGAAACAACGTCAGGAACCTAAGGGAAAGCTGAGGCTACCCC----- 52740

Qy 1160 CCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACCCCATCTCCTCAGCTACAC 1219  
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Db 52739 -----CAC 52737

Qy 1220 CTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACCACCTCCAGCCCCAGCACC 1279  
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Db 52736 GCCAAACTCTATTCCCTGTCCCTACCTCCGTCACCTACACCCCATTC-----CC 52682

Qy 1280 AGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCCAACCCACCTCATCTCTCTCA 1339  
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Db 52681 CACCCCATCCCTACCGGCACCTCTATCCACATCCCCCA----- 52643

Qy 1340 TGTGCCCCACTCCCATCGCCTCCCCCATCTGTCGAGAATCCGGTT-TGCCCCCTGCTCTCA 1398  
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Db 52642 -----CCCCTATCTGTCGAGAATCCGATTCTGCCCCCTGATTTC 52604

Qy 1399 ACCCAGGGAAGCCCTGGTAGGCCCCGATGTGAAACCACTGACTTGAACCTCACAGATCTGA 1458  
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Db 52603 ACCCAGGGAAGCCCTAGGGGGCCCGATGTGATGCTGCTGACTTGTGCATTGCGGGTCAGA 52544

Qy 1459 GAGAAGCCAGGTTTCATTTAATGGTTCTGAGGGGCGGCTTGAGATCCACTGAGGGGAGTGG 1518  
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Db 52543 GAGAATCAAGG-----GCATGGTTCTGAGAAGCCGACTGAGATCAGCAGAGGGGAATGG 52490

Qy 1519 TTTTAGGCTCTGTGAGGAGGCAAGGTGAGA-TGCTGAGGGAGGACTGAGGAGGCACACAC 1577  
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Db 52489 GCCCGGGCTCTGTGAGGAGGCAAGGTGAGACCCCCGAGGAAGGAATGAGGAAGCCCTCAC 52430

Qy 1578 CCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTGCCAGCCCTGGACCACCC 1637  
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Db 52429 CCA--GATAGAGAACCCCAAATAATCCAGTACTACCTTTGCTGCCAGCCCTGGACCAC-- 52374

Qy 1638 GGCCAGGACAGATGTCTCAGCTGGACCACCCCCCGTCCCGTCCCACTGCCACTTAACCCA 1697  
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Db 52373 --CCAGGGCAGACTTCTCAGGCTGGACCTTCCC--CCCTCCCCACTGCCACTTAAGCCA 52319

Qy 1698 CAGGGCAATCTGTAGTCATAGCTT-ATGTGACCGGGGCAGGGTTGGTCAGGAGAGGCAGG 1756  
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Db 52318 CAAGGGACTCTGGAGTCAGACCTTGGTGTGACCAGGGAAGGGCCGGTCAGGAGAGG---- 52263

Qy 1757 GCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGGACCTGGGAGGGAACT 1816  
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Db 52262 -----GCAGGGGCCAGGCTCTGTGAGGCATCAAAATCAGGACCCTGAGAGAGAATT 52212

Qy 1817 GAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACCCCACTCACATTCCCAT 1876  
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Db 52211 GAGGGCCCCACCCCAACCCCTATACCCATCCCTAACCCCATACCCACTCTACTTGCATT 52152

Qy 1877 ACCTACCCCTACC-----CCCAACCTCATCTTGTGAGAA-----TCCCTGCTGTC 1922  
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Db 52151 CCCAGCCCCATCCCCACACCTACCCCATCTTGGCAGAATCTGTTTCTTTCCCTGCAGTC 52092

Qy 1923 AACCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCAGG 1982  
| | | | | | | | | | | | | | | | | | | | | |

Db 52091 AACCACAGAAGCCCCAGGAATGACAGACAGGCACACCCATTCTGACGTCCACATCCAGG 52032

Qy 1983 GTCTGATGGAGGGAAGGGGCT-----TGAACAGGGCCTCAGGGGAGCAGAGGGAGG-- 2033  
| | | | | | | | | | | | | | | | | | | | | |

Db 52031 GCTGAAGGAGGGAAGGGCTTAGTATCATGAGCAGGGCCTCAGGGGAGTCTCTGCTCCTC 51972



Qy	2034	--GCCCTACTGCGAGATGAGGGAGGCGCTCAGAGGACCCAGCACCTAGGA-----C	2082
Db	51971	AAGCCCTGCTGGGAGTAAAGGGAGGCGCTCAGGGAACCCAGGTCCCTCAGGATAGGGGGTCC	51912
Qy	2083	ACCGCACCCCTGTCTGAGACTGAG--GCTGCCACTTCTGGCCTCAAGAATCAGAACGATG	2140
Db	51911	ACTCCAACCCTGTCTGAGACTGAGGCGCCTCCTCTTTCATCCTCGGGAATCAGAGGGATG	51852
Qy	2141	GGGACTCAGATTGCATGGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGA	2200
Db	51851	GAGACTCACGTCAGCAGAGGGTGGGGCCCAACCCTGCCAGGATCAAGGAGAGGAAGAAGA	51792
Qy	2201	GGGAGGACTCAGGGGACCTTGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCA	2260
Db	51791	GGGAGGACTCAGGGTACCTTTGAGTCCAGAACAATGGGGACCTTTGCCCTGGGAGGTCCA	51732
Qy	2261	GGGCACGGTGGCCACATATGGCCCATATTTCTTGCATCTTTGAGGTGAC----AGGACAG	2316
Db	51731	GTGCACAGTGGCCACCTGTAGCCCATGCTTGCTGCACCTTCTGGGTGACAAAGAGGAGAG	51672
Qy	2317	AGCTGTGGTCTGAGAAGTGGGGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATAT	2376
Db	51671	GGCTGTGGTCAGAGCAGTGGTGACTCAGGTCAAGAGAGGGAGGAGTCCAGCATCTGCAG	51612
Qy	2377	GGCCCAAGATGTGCCCCCTTCATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGAC	2436
Db	51611	GCCCCAATGTGTGCCCCATTCATGAAGATTGGGGATA-CCTTGGCTCAGAAAGAAGGGAC	51553
Qy	2437	TCCACACAGTCTGGCTGTCCCCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGG	2496
Db	51552	CCCACAGAGTCTGGCTGTCCCCTGATTTTTGCTCAGAGGGGACCAAATCAAGGATAGCCC	51493
Qy	2497	TATGTTCCATTCTCACTTGTACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGG	2556
Db	51492	TATGTGCCAACCTCATTGTGCCACAGGAAAGAAGTTGAAGAGCCCTCAGGGTGATGGGG	51433
Qy	2557	TCTTGGGGTAAAGGGGGGATGTCTACTCATGTACAGGAATTGGGGGTTGAGGAAGCACAG	2616
Db	51432	TCTTGCAGTAAAGGGGAGCTATCTGCTCATCTCAGGGGGTTTCAGGTTGAGGAATGGCAG	51373
Qy	2617	GCGCTGGCAGGAATAAAGATGAGTGAGACAGACAAGGCTATTGGAATCCACACCCAGAA	2676
Db	51372	GCCCCATCACG----ATGAAGAGTAACCCACAGGAGGCCATAGAAACACTACCCACAGAA	51317
Qy	2677	CCAAAGGGGTCAGCCCTGGACACCTCA-----CCCAGGATGTGGCTTCTTTTTCAC	2727
Db	51316	CCAAAGGGGTCATACCTGGACACCCCATGTGGGGGTGACAGGATGTAGC-TCCATCTCAT	51258
Qy	2728	TCCTGTTTTCCAGATCTGGGGCAGGTGAGGACCTCATTCTCAGAGGGTGACTCAGGTCAAC	2787
Db	51257	TCCTGTTTTCCAGATCTCGGGGAGGTGAGGAACCTGTTCTCCAGGATGACTCAGGTCAAC	51198
Qy	2788	GTAGGGACCCCATCTGGTCTAAAGACAGAGCGGTCCAGGATCTGCCATGCGTTCGGGT	2847
Db	51197	ACAGGGGCCCCCATCTGGTGGATAGACAGAGTGGTCCAGGATCTGTCTAGTAGTTCCGGT	51138
Qy	2848	GAGGAACATGAGGGAGGACTGAGGGTACCCAGGACAGAACACTGAGGGAGACTGCACA	2907
Db	51137	GAGGAACATGAGGGACGATTGAGGGCACCCCTTGGGCCAGAACACAGATGAGGACCTCACG	51078

Qy	2908	GAAATCAGCCCTGCCCTTGCTGTCAACCCAGAGAGCATGGGCTGGGCCGTCTGCCGAGGT	2967
Db	51077		
		GAAATCTGCCCTGCCCTTGCTGTCTACTCCAGAGAGCATGGGCAGGGCTGTCTGCTGCAGT	51018
Qy	2968	CCTTCCG--TTATCCTGGGATCATTGATGTCAGGGACGGGGAGGCCCTTGGTCTGAGAAGG	3025
Db	51017		
		CCCCCGACTTACCTTGGGATCATTGGTGTGTCAGGGATGGGGAGGTCTTTGTC-GAGGGGT	50959
Qy	3026	CTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACCA	3085
Db	50958		
		CTGCACTCAGGTCAGTAGAGGGAGCGTCTTAGGCCCTGCCAGGAGACAAGGTAAGAACGA	50899
Qy	3086	AGCGGGCACCTCACCCAGGACACATTAATTCCAATGAATTTGATATCTCTTGCTGCCCT	3145
Db	50898		
		AGCAGGTTCTCACCCAGGACACATGAATTCCAATGCATTTCAGCATCTCTTCCTGTCT	50839
Qy	3146	TCCCCA-AGGACCTAGGCACGTGTGGCCAGATGTTTGTCCCTCCTGTCTTCCATTCT	3204
Db	50838		
		TCCAAGAGGACCTGGGCACGTGTGGCCAGATGTGAGTCTCTCATGTCTCT--GTTCCC	50782
Qy	3205	TATCATGGATGTGAACCTCTTGATTGATTCTCTCAGACCAGCAAAAGGGCAGGATCCAGG	3264
Db	50781		
		TATCAGGGATGTGAGCTCTTAATCTGAGTTTCTCAGGCCAGCAAAAGGGTGGGATCCAGG	50722
Qy	3265	CCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCCACTGCATGA	3324
Db	50721		
		CCTTGCCAGGAGAAAGGTGAGGGCCCTGTGTGAGCACAGAGGGGACCATTACCCCAAGA	50662
Qy	3325	GAGTGGGGATGTACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGCCAGGGCTGT	3384
Db	50661		
		GGGTGGAGACCTCACAGATTCCAGCCTACCCTCCTGTTAGCACTGGGGCCTGAGGCTGT	50602
Qy	3385	GCTTGCGGTCTGCACCTGAGGGCCCGTGGATTCTCTTCTTCCAGCTCCAGGAACCAGG	3444
Db	50601		
		GCTTGCACTCTGCACCTGAGGGCCCATGCATTCTCTTCCAGGAGCTCCAGGAAACAGA	50542
Qy	3445	CAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATGCACAG----	3500
Db	50541		
		CACCTGAGGCCTTGGTCTGAGGCCGTGCCCTCAGGTCACAGAGCAGAGGAGATGCAGACGT	50482
Qy	3501	GGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCACAGGA	3560
Db	50481		
		CTAGTGCCAGCAGTGAACGTTTGCTTGAATGCACACTAATGGCCCCCATCGCCCCAGAA	50422
Qy	3561	CACATAGGACTCCACAGAGTCTGGCCTCA-CCTCCCTACTGTGAGTCTCTGTAATCGAC	3619
Db	50421		
		CATATGGGACTCCAGAGCACCTGGCCTCACCTCTCTACTGTGAGTCTCTGAGAATCAGC	50362
Qy	3620	CTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCTTCTCAGGTTTTCAGGGGA	3679
Db	50361		
		CTCTGCTTGTGTTGTGTACCCTGAGGTGCCCTCTCACTTTTCTTCTCAGGTTCTCAGGGGA	50302
Qy	3680	CAGGCCAACCCAGAGGAC-----AGGATTCCCTGGAGGCCACAGAGGAGCAC	3726
Db	50301		
		CAGGCTGACCAGGATCACCAGGAAGCTCCAGAGGATCCCCAGGAGGCCCTAGAGGAGCAC	50242
Qy	3727	C-AAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTG	3785
Db	50241		
		CAAAGGAGAAGATCTGTAAGTAAGCCTTTGTTAGAGCCTCCAAGGTTTCAGTTTTCAGCTG	50182
Qy	3786	AGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCACGCTCCTGC	3845

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Db      50181 AGGCTTCTCACATGCTCCCTCTCTCTCCAGGCCAGTGGGTCTCCATTGCCCAGCTCCTGC 50122
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Qy      3906 ACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGC 3965
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Db      50061 ACTGCAAGCCTGAGGAAGGCCCTTGACACCCAAGAAGAGGCCCTGGGCCTGGTGGGTGTGC 50002
Qy      3966 AGGCTGCCAC-----CTCCTCCTCCTCTCCTCTGGTCTGGGCA 4004
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      50001 AGGCTGCCACTACTGAGGAGCAGGAGGCTGTGTCTCTCCTCTCCTCTGGTCCCAGGCA 49942
Qy      4005 CCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCT 4064
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Db      49941 CCCTGGGGGAGGTGCCCTGCTGCTGGGTCAACAGGTCTCTCAAGAGTCCTCAGGGAGCCT 49882
Qy      4065 CCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCA 4124
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Db      49881 CCGCATCCCCACTGCCATCGATTTCATCTATGGAGGCAATCCATTAAGGGCTCCAGCA 49822
Qy      4125 GCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCTTGTTCGAGCAGTAA 4184
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      49821 ACCAAGAAGAGGAGGGGCCAAGCACCTCCCCTGACCCAGAGTCTGTGTTCGAGCAGCAC 49762
Qy      4185 TCAC TAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGC 4244
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Db      49761 TCAGTAAGAAGGTGGCTGACTTGATTCTTTCTGCTCCTCAAGTATTAAGTCAAGGAGC 49702
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Qy      4305 AGATCTTCGGCAAAGCCTCTGAGTCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAG 4364
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Db      49581 CGGACCCACAGCAACACCTTACACCTTGTCACCTGCCTGGG--ACTCCTATGATGGCC 49524
Qy      4425 TGCTGGGTG---ATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCA 4481
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Db      49463 TGATTGCAATGGAGGGCAAATGCGTCCCTGAGGAGAAATCTGGGAGGAGCTGAGTGTGA 49404
Qy      4542 TGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCC 4601
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Db      49403 TGAAGGTGTATGTTGGGAGGGAGCACAGTGTCTGTGGGGAGCCCAGGAAGCTGCTCACCC 49344
Qy      4602 AAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCAC 4660
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Db      49343 AAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCAGCAGTGATCCCATAT 49284
Qy      4661 GCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCTCTTG 4720
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Db	49283	GCTATGAGTTACTGTGGGGTCCAAGGGCACTCGCTG-----CTTGAAAGTACTGG	49234
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Db	49233	AGCACGTGGTCAGGGTCAATGCAAGAGTTCTCATTTCTACCCATCCCTGCATGAAGCAG	49174
Qy	4781	CTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGG	4840
Db	49173	CTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGCTGCAGCCAGGGCCACTGCGAGGG	49114
Qy	4841	GGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCC-TCGTGTGAC	4899
Db	49113	GGGCTGGGCCAGTGCACCTTCCAGGGCTCCGTCCACTAGTTTCCCCTGCCTTAATGTGAC	49054
Qy	4900	ATGAGGCCCATTCCTTCACTC--TGAAGAGAGCGGTGAGTGTCTCAGTAGTAGGTTTCTG	4957
Db	49053	ATGAGGCCCATTCCTTCTCTCTTTGAAGAGAGCAGTCAACATTCTTAGTAGTGGGTTTCTG	48994
Qy	4958	TTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTT	5017
Db	48993	TTCTATTGGATGACTTTGAGATTTGTCTTTGTTTCCTTTTGAATTGTTCAAATGTTCC-	48935
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Qy	5077	-AGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCC	5135
Db	48874	TAGTGCTGTTTATATAGTTTAGGAGTAAGAGTCTTGTTTTTTATTTCAGATTGGGAAATCC	48815
Qy	5136	ATTCTATTTTTGTGAATTGGG--ATAATAACAGCAGTGGAATAAGTACTTA-GAAATGTGA	5192
Db	48814	ATTCCATTTTGTGAATTGGGACATAGTTACAGCAGTGGAATAAGTATTCATTTAGAAATG	48755
Qy	5193	AAAATGAGCAGTAAATAGATGAGATAAAGAACATAAGAAATTAAGAGATAGTCAATTCT	5252
Db	48754	TGAATGAGCAGTAAACTGATGACA-----TAAAGAAATTAAAGATATTTAATTCT	48703
Qy	5253	TGCCTTATACCTCAGTCTATTCTGTAAAA--TTTTTAAAGATATATGCATACCTGGATTT	5310
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Qy	5311	CCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAGAATTCTTCCTGTTCA	5370
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Qy	5371	CTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTTGAAGGCCCTGGGTTAGTAG	5430
Db	48583	CTGGCTCATTTATCTCTATGCACTGAGCATTGCTCTGTGGAAGGCCCTGGGTTAATAG	48524
Qy	5431	TGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCT	5490
Db	48523	TGGAGATGCTAAGGTAAGCCAGACTCACCCCTACCCACAGGGTAGTAAAGTCTAGGAGCA	48464
Qy	5491	GCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAGGGAAAAGTGAGAGAGG	5550
Db	48463	GCAGTCATATAATTAAGGTGGAGAGGTGCCCTCTAAGATGTAGAGAAAAAGTAAGAAAGG	48404
Qy	5551	GGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGCCCTGAGCTGGGGCAT	5610
Db	48403	GGTGAGGGTGTGGGGCTCCAGGTGAGAGTGGTCCAGAGGTAAATGCCCTGTGTGGGGCCT	48344

Qy 5611 TTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGG 5670  
|||||  
Db 48343 TTTGGACTTTGGGAAACTGCAGTTTCTTCGGAGGGAGCTGATTCTAATGAATCGGCGGGG 48284

one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

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Neighboring sequence information:

This clone is overlapped by RP11-366F6, Qc-7G11, RP1-77B24, ICRFXc104-E0681, Qc-11C8, RP11-329E24, RP11-173J18, Qc-3H5, Qc-3G5, Qc-16C3 and covers Qc-9A9, RP1-73F14 entirely.

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Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

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FEATURES

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Qy	520	ACCC---CACTCCCGTGACCCAACCCCCACTCCAATGCTCACTCCCGTGACCCAACCCCC	576
Db	160642	CCCCATTCCCATCCCCCACCACATCCCCATTTCATCCCCATCCCCACCTCCATCCCCCA	160583
Qy	577	TCTTCATTGTCATTCCAACCCCCACCCACATCCCCCACCACATCCCTCAACCCTGATGC	636
Db	160582	CCAGAACCCTATCCCCCACCAGAAACCCTATCCTGCCCCACTCCCCACCACGTTTCATCCC	160523
Qy	637	CCATCCGCCCA-GCCATTCCACCCTCACCCCCACCCCCACCCCCACGCCACTCCACCC	695
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Qy	743	GATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGAGAAGCGAGTTTCCATTCTGAG	802
Db	160402	GATGTGGTGCCACTGTCTTGACATTTGAGGTCGGAGAGAAGCAAGGGCTCGCTCTCAG	160343
Qy	803	GGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCAGGCTCTGTGAGGAGGCAAGGTGAG	862
Db	160342	GGGCAGC-TGGAGATCAGCTGAGGGCAGCTGGCCCTGGCTCTGTGAGGATGCAAGGTGAG	160284
Qy	863	AGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATAGAGAGCCCCAAATATTCCAG--	920
Db	160283	ATGCTGAGGGAGGACTAAGGAGTATCCACCCCTGGTAGTGAGCCCCAAATAATCCAGTG	160224
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Qy	1040	TCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGGGCAGGGCACAGGCTCTGCC	1099
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Qy	1160	CCCACTCCCAACCCATTGCGATTCCCATTCCTCCCAACCCCCATCTCCTCAGCTACAC	1219
Db	160021	-----CAC	160019
Qy	1220	CTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACCACCCTCCAGCCCCAGCACC	1279
Db	160018	GCCAAACTCTATTCTGTCCCTACCTCCGTCCCCACCTACACCCCCCATTC-----CC	159964
Qy	1280	AGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAACCCACCTCATCTCTCTCA	1339
Db	159963	CACCCCATCCCTACCGGCACCTCTATCCACATCCCCCA-----	159925

Qy 1340 TGTGCCCCACTCCCATCGCCTCCCCCATTCTGGCAGAATCCGGTT-TGCCCCCTGCTCTCA 1398  
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 Db 159313 GCTGAAGGAGGGAAGGGCTTAGTATCATGAGCAGGGCCTCAGGGGAGTCTCTGCTCCTC 159254  
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Db	159073	 GGGAGGACTCAGGGTACCTTTGAGTCCAGAACAATGGGGACCTTTGCCCTGGGAGGTCCA	159014
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Qy	2317	AGCTGTGGTCTGAGAAAGTGGGGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATAT	2376
Db	158953	GGCTGTGGTCAGAGCAGTGGTGACTCAGGTCAGCAGAGGGAGGAGTCCCAGCATCTGCAG	158894
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Db	158893	GCCCCAATGTGTGCCCATTCATGAAGATTGGGGATA-CCTTGGCTCAGAAAGAAGGGAC	158835
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Qy	2617	GCGCTGGCAGGAATAAAGATGAGTGAGACAGACAAGGCTATTGGAATCCACACCCCAGAA	2676
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Db	158598	CCAAAGGGGTCATACCTGGACACCCCATGTGGGGGTGACAGGATGTAGC-TCCATCTCAT	158540
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Db	158539	TCCTGTTTTCAGATCTCGGGGAGGTGAGGAAC TTGTTCTCCGAGGATGACTCAGGTCAAC	158480
Qy	2788	GTAGGGACCCCCATCTGGTCTAAAGACAGAGCGGTCCCAGGATCTGCCATGCGTTCGGGT	2847
Db	158479	ACAGGGGCCCCCATCTGGTGGATAGACAGAGTGGTCCCAGGATCTGTCAGTAGTTCCGGT	158420
Qy	2848	GAGGAACATGAGGGAGGACTGAGGGTACCCAGGACCAGAACACTGAGGGAGACTGCACA	2907
Db	158419	GAGGAACATGAGGGACGATTGAGGGCACCTTGGGCCAGAACACAGATGAGGACCTCACG	158360
Qy	2908	GAAATCAGCCCTGCCCCCTGCTGTCACCCCAGAGAGCATGGGCTGGGCCGTCTGCCAGGT	2967
Db	158359	GAAATCTGCCCTGCCCCCTGCTGTCACTCCAGAGAGCATGGGCAGGGCTGCTGCTGCAGT	158300
Qy	2968	CCTTCCG--TTATCCTGGGATCATTGATGTGAGGGACGGGGAGGCCTTGGTCTGAGAAGG	3025
Db	158299	CCCCCGACTTACCTTGGGATCATTGGTGTGAGGATGGGGAGGTCTTTGTC-GAGGGGT	158241
Qy	3026	CTGCGCTCAGGTCACTAGAGGGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACCA	3085
Db	158240	CTGCACTCAGGTCACTAGAGGGAGCGTCTTAGGCCCTGCCAGGAGACAAGGTAAGAACGA	158181
Qy	3086	AGCGGGCACCTCACCCAGGACACATTAATTCCAATGAATTTTGATATCTCTTGCTGCCCT	3145

Db 158180 AGCAGGTTTCCTCACCCAGGACACATGAATTCCAATGCATTTTCAGCATCTCTTCCTGTCTCT 158121

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Db 158120 TCCCAAGAGGACCTGGGCACGTGTGGCCAGATGTGAGTCTCCTCATGTCTCT---GTTCCC 158064

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Db 157643 CTCTGCTTGCTTGTGTACCTGAGGTGCCCTCTCACTTTTTCTCCTTCAGGTTCTCAGGGGA 157584

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Db 157523 CAAAGGAGAAGATCTGTAAGTAAGCCTTTGTTAGAGCCTCCAAGGTTCACTTTTCTAGCTG 157464

Qy 3786 AGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGC 3845  
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Qy 3846 CCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGC 3905  
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Qy	4125	GCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGGAGCAGTAA	4184
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Qy	4245	CAGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTTG	4304
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Qy	4425	TGCTGGGTG---ATAATCAGATCATGCCAAGACAGGCTTCCTGATAATTGTCCTGGTCA	4481
Db	156805	TGGTGGTTGATAATAATCAGATCATGCCAAGACGGGCTCCTGATAATCGTCTTGGGCA	156746
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Qy	4900	ATGAGGCCCATTTCTTCACTC--TGAAGAGAGCGGTGAGTGTTCCTCAGTAGTAGGTTTCTG	4957
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Qy	5077	-AGTTCGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCC	5135
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Qy	5193	AAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCT	5252
Db	156036	TGAATGAGCAGTAAAAC TGATGACA-----TAAAGAAATTAAGATATTTAATTCT	155985
Qy	5253	TGCCTTATACCTCAGTCTATTCTGTAAAA--TTTTTAAGATATATGCATACCTGGATTT	5310
Db	155984	TGCCTTATA-CTCAGTCTACTCGGTAAATTTTTTTTAAAAAATGTGCATACCTGGATTT	155926
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Qy	5431	TGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGTC TAGGAGCT	5490
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Qy	5551	GGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTC AATGCCCTGAGCTGGGGCAT	5610
Db	155685	GGTGAGGGTGTGGGGCTCCAGGTGAGAGTGGTCCAGAGGTAAATGCCCTGTGTGGGGCT	155626
Qy	5611	TTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGG	5670
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ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 11495)  
 AUTHORS Kipps,T.J. and Wu,Y.  
 TITLE Vaccines with enhanced intracellular processing  
 JOURNAL Patent: US 6287569-A 9 11-SEP-2001;  
 FEATURES Location/Qualifiers  
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 ORIGIN

Query Match 46.8%; Score 2655; DB 2; Length 11495;  
 Best Local Similarity 73.6%; Pred. No. 0;  
 Matches 4231; Conservative 0; Mismatches 1100; Indels 416; Gaps 50;

Qy	21	CCTCCCCCTACCACCCCCAATCCCTCCCTTTACGCCACCCATCCAAACATCTTCACGCTC	80
Db	5969	CCAGCACCCCTATCCTCCCCAAACCCCACTACCTTATGTCTCATCCCCACCCCAAC	6028
Qy	81	ACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTGCTCTCAACCCAGGGAAGC-C	139
Db	6029	ACCACATATCCCATCCAGGTTGAATCGCATTCGTTTCTGCTTCAACCCAGGGAAGCTC	6088
Qy	140	CAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGGTTAGAGAGAAGCGAGGTTT	199
Db	6089	CAGGTTCTTGGATGTGATGCCAGTGACTTGTGCATTGGGGGTTAGAGAGACGCTAGCTTC	6148
Qy	200	TCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGGCCCA-GCTCTGTAAGGAGG	258
Db	6149	TCAGTCTGACAGGCAGCTTGGGATTGGCAGAGGGAAGCCGGTCCAGGCTCTGTGAGGTGG	6208
Qy	259	CAAGGTGACATGCTGAGGGAGGACT---GAGGACCCACTTACCCAGATAGAGGACCCCA	315
Db	6209	CATAGTGAGAAGCTGAGGGAGAAGTCGGGAGGCCCTCTCCACCCAGATAGACGACCCCA	6268
Qy	316	AATAATCC-----CTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTCTCAGGC	366
Db	6269	AATAATCCGGCACCCCTCCTGCTTCCAGTCCTGGGCCACCCGTGGGCGGACTTCTGAGTC	6328
Qy	367	TGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAGCTCCGT	426
Db	6329	TGGGACGCCCACCACCCCACTGCCGCTGAAGCCGCAGGGACTATGGAGTCAGAGCTTGGT	6388
Qy	427	GTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACATCATGCT	486
Db	6389	GTGATCAGTGCAGGACTGGTGGGGT-----AGGCTCTGCCAGGCATCAACGT	6436
Qy	487	CAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAACCCCCAC	546
Db	6437	CAGGACCCTAGGAGAGGGCTGAGTGTCCCCA---CCCCATTCTATCCCCTACCCCTT	6493
Qy	547	TCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCAACCCAC	606
Db	6494	TCCCATCTGCACTCCC-----TACCCCATCTGTACCCCC	6527
Qy	607	ATCCCCCAACCCATCCCTCAACCCCTGATGCCCATCCGCCAGCCATTCCACCCCTACCCC	666
Db	6528	ATTCCCCACCTGTGCCCCATCCTCCCCAACCCCCCAACCAGCCTCATACCCCTCCCC	6587
Qy	667	CACCCCCACCCCAAGCCCACTCCCAACCCCAACCCAGGCAGGATCCG-GTTCGCCAGG	725

Db	6588	CACCCCTACCTTCATCCCCATCAGTGCAGCATCCGGTTCCACCCCTGCTTTCAATCCAGG	6647
Qy	726	AAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGAGAAGC	785
Db	6648	CAAGCCCTGGGTGGCCGGATGTGATGCCACTGACTTGTGAATTGAGGGTTAGAGAGAAGT	6707
Qy	786	GAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGGCTCTG	845
Db	6708	GAGTTTCTGGGTCTGAAGGGTGGC-TTGAGATCGGCAGAGGGAAGGTGGCCAGGCTTTG	6766
Qy	846	TGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAATAGAGAG	905
Db	6767	TGAAGAGGCAAAGTGAGACTCTGAGGGAGGATTCAGGAAACCCTATCCCTGATAGAGGG	6826
Qy	906	CCCCAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGACGTCT	965
Db	6827	TCCCAGCCCTGGACTACCC-----CGCGGAGGCTGACTTCT	6862
Qy	966	CAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTCTTCTC	1025
Db	6863	CAGACTGGGCTGCTCCCCACCTCCGCCCCC-----TTCGCAACGCGTTTGTTTAAGCCAC	6917
Qy	1026	CCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGGGCAGG	1085
Db	6918	AGGGGACTCTGGAGTCAGAGGTTGGTGTGATCAGGGAAGGGCTGGTTAGGAGA-GGCATG	6976
Qy	1086	GCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCCCCAAG	1145
Db	6977	GCCCAGGCCCTGCCAGGAATCAAAGTCAGAAACC-TGAGAGGGAAC TGAGGTCCCCCAAG	7035
Qy	1146	ACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACCCCAT	1205
Db	7036	ATCCTAGTCTAACCCCCACTCCCACAA-----	7062
Qy	1206	CTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACCACCT	1265
Db	7063	-----ATCCGCTGCCATTTCGCTGCTCCATTCCCATTCTTGCCCT	7104
Qy	1266	CCAGCCCCCAGCACAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCCAACCCAC	1325
Db	7105	CCACCCTCACCA-----	7116
Qy	1326	CCTCATCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATTCGGCAGAATCCGGTTT	1385
Db	7117	-----GGCAGAATCCAGTTC	7131
Qy	1386	GCC-CCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACTTGAA	1444
Db	7132	CCCTTCTGCTATCAATCCAGGGAACCCAGGCTTGGTGCTGGGATGTTTT-----	7183
Qy	1445	CCTCACAGATCTGAGAGAAGCCAGGTTCAATTAATGGTTCTGAGGGGCGGCTTGAGATCC	1504
Db	7184	-----TGGGGGTCAGAGAATCAAGGGCATAGTCC TGAGGGGCCAGTTGAGATCG	7232
Qy	1505	ACTGAGGGGAGTGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGGACTG	1564
Db	7233	GCTGAGGGGAGCGGGCCCAAGCTCTGTGGCAGGCAAGGTGAGACTCTGAGGAAGGACTG	7292
Qy	1565	AGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTGCCAG	1624



Db	7293	AGGAGGCCCCCACCAAGATAGA-GGAACCCAAATAATCCAGCGCAGCTCCTGCTGCCAG	7351
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Db	7352	TCCTGGACCACCCGG---GGGAAGACTTCTCA---GGCTAGGCCATCCCAGCTCCCCT	7404
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Db	7405	GCCACTAAAGCTACAGGGGACTCTAGAGTCAAGAGCTTGGTGTGCCCA-----	7452
Qy	1745	AGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCCGCATTAGGGTCAGGACCC	1804
Db	7453	-----AGGCAGGGCCAGGC-----TCTGCCTGGCATCGGGGTCAGGACCT	7493
Qy	1805	TGGGAGGGAAGCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACCCAC	1864
Db	7494	TGAGAGGGAAGCTGAGGGCGCTACACCCCAACCCATCCGCATTC-----CAACAT	7543
Qy	1865	TCACATTCCCATACTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTGTCAA	1924
Db	7544	GCCCAGCCCCATCCCCAACTCCGTTTGCAGAATCCATTTT---TCCCTGCAGTCAA	7599
Qy	1925	CCCACGGAAGCCACGGGAATGGCGGCCAGGCCTCGGATCTTGACGTCCCCATCCAGGGT	1984
Db	7600	CCCCGGGAAGACCTGGGAATGGT---CAGGCCTCGGATCTTGACATCCACATCGAGGGC	7656
Qy	1985	CTGATGGAGGGAAGGGG-----CTTGAACAGGGCCTCAGGGGAGCAGAGGGAG-----	2032
Db	7657	TGAAGGAGGGAGAGGGTTTGGTATCATGAGCAGAGCCTCAGGGTAGCAGAGGGAGGACCC	7716
Qy	2033	-GGCCCTACTGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCC-----TAGGAC	2082
Db	7717	TGGCCCTCCTGGGAGATGAGGAAGGCCTCAGGAGACCCAGCACCCCAAGGCAGGGAGCCC	7776
Qy	2083	ACCGCACCCCTGTCTGAGACTGAG--GCTGCCACTTCTGGCCTCAAGAATCAGAACGATG	2140
Db	7777	ACCCACCCCTGTCTGAGAATGAGGTGCCTCCTCTTTTAGCCTCAGGAATCCAAGGGATG	7836
Qy	2141	GGGACTCAGATTGCAT--GGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAG	2198
Db	7837	GCAACTCAGGTCAGCAGAGGGGTGGGTCCAAGCCCTTCCAGGATCAAGGAAAGGAAGAC	7896
Qy	2199	GAGGGAGGACTCAGGGGACCTTGGGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTC	2258
Db	7897	GAGGGAGGATTACGGGGGCCTTGCAATCCAGATCAGTGGAGACCTGGGCCCTGGGAGGTC	7956
Qy	2259	CAGGGCACGGTGGCCACATATGGCCCATATTTCTGCATCTTTGAGGT---GACAGGAC	2314
Db	7957	CTGGGCAAGGTAGCCACCTGTAGCTCATACTTCTGCATCTTCGAGGTCACAGAGAGGAG	8016
Qy	2315	AGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCAT	2374
Db	8017	AGGGCTATGGTCTGAGGGGTGGTACTTCAGGTCCGCAGAGGGAGGAGTCCAGGATCTAC	8076
Qy	2375	ATGGCCCAAGATGTGCC-CCCTTCATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGG	2433
Db	8077	AGGACCCAAGGTGTGCCACACTTCACGAGGAATGGGGATACCTGTGGCTCAGAAAGACGG	8136
Qy	2434	GACTCCACACAGTCTGGCTGTCCCCTTTTAGTAGCTCTAGGGGGACAGATCAGGGATGG	2493
Db	8137	GACCCACAGAGTCTGGCTGTCCCTGTCTTAGCTCAGGGGGGACAGAGGAGGGATGG	8196

Qy	2494	CGGTATGTTCCATTCTCACTTGTACACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATG	2553
Db	8197	CCCATATGTGCCAATTTCACTTGTTCACAGGCAGGAAGTTGGGGAACCTTCAGGGAGATG	8256
Qy	2554	GGGTCTTGGGGTAAAGGGGGGATGTCTACTCATGTTCAGGGAATTGGGGGTGAGGAAGCA	2613
Db	8257	AGGTTTGGAGTAAAGGGGCAATGTTTGCTCATCTCAGGGGTTGGGGGTGAGGAAGGG	8316
Qy	2614	CAGGCGCTGGCAGGAATAAAGATGAGTGAGACAGACAAGGCTATTGGAATCCACACCCCA	2673
Db	8317	CAGGCCCTGTCAGGAGCAAACATGAGT-ACCCACAGGAGGCCATCAGAACCCTCACCCCA	8375
Qy	2674	GAACCAAAGGGGTGAGCCCTGGACACCTCACCCAG-----GATGTGGCTTCTTTTTTC	2725
Db	8376	GAACCAAAGGGGTGAGCCCTGGGCACCCACACAGGGGTGACAGGATGTGGCTCCTTCTC	8435
Qy	2726	ACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCTCATTCTCAGAGGGTGACTCAGGTCA	2785
Db	8436	ATTTCGTATTCCAGATCTCAGTGAGGTGAGGACCTTGTTCTCAGAGGGTGACTCAGGTCA	8495
Qy	2786	ACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCGGTCCCAGGATCTGCCATGCGTTCGG	2845
Db	8496	CCACAGGGACCCCCATCTGGTCTACAGACACAGTGGTCCCAGGATCTGCCAAGAGTCCTG	8555
Qy	2846	GTGAGGAACATGAGGGGAGGACTGAGGGTACCCAGGACCAGAACACTGAGGGGAGACTGCA	2905
Db	8556	GTGAGGAATGTGAGGGGAGGATTGAGGGTACCACAGGGCCAGAACGCAGATGATGACCCCA	8615
Qy	2906	CAGAAATCAGCCCTGCCCCTGCTGTACCCAGAGAGCATGGGCTGGGCCGTCTGCCGAG	2965
Db	8616	CAGAAATCAGCCCTGCTCCTGTTGTCACCCAGAGAGCATGGGCTTGCTTTCTGCTGAG	8675
Qy	2966	GTCCTTCGTTATCCTGGGATCATTGATGTCAGGGACGGGGAGGCCTTGGTCTGAGAAGG	3025
Db	8676	GTCCCTCTCTTATCCTGGGATCACTGGTGTACGGAGTGGGAGGCCTTGGTCTGAGGGGG	8735
Qy	3026	CTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACCA	3085
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Qy	3086	AGCGGGCACCTCACCCAGGACACATTAATTCCAATGAATTTTGATATCTCTTGCTGCCCT	3145
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Qy	3146	TC-CCCAAGGACCTAGGCACGTGTGGCCAGATGTTTGTCCCTCCTGTCCTTCCATTCCCT	3204
Db	8856	TCTTCGGAAGACCTAGGCACAGGTGGCCAGATGTGGGGTTTCTTAGGTCTCT---GTTCC	8912
Qy	3205	TATCATGGATGTGAACTCTTGATTGGATTCTCAGACCAGCAAAAGGGCAGGATCCAGG	3264
Db	8913	TCTCAGGCATGTGAGCTCTTGATCTGAGTTCTCAGGCCAGCAAAAGAGTGGGATCCAGG	8972
Qy	3265	CCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCCACTGCATGA	3324
Db	8973	CCCTGCCTGGAGAAATGTGAGGGCCCTGAGTGAACACAGTGGGGATCATCCACTCCATGA	9032
Qy	3325	GAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGCCAGGGCTGT	3384
Db	9033	GAGTGGGGACCTCACAGAGTCCAGCCTACCCTCTTGATGGCACTGAGGGACCGGGGCTGT	9092

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Db	9093	GCTTAC	AGTCTG	CACCTA	AGGGCC	CATGG	ATTTC	CTTC	TAGG	AGCTCC	AGGA	ACAAGG	9152
Qy	3445	CAGTG	AGGCCT	TGGTCT	GAGAC	AGTAT	CCTC	AGGT	CAC	AGAG	CAGAG	GATGC	3504
Db	9153	CAGTG	AGGCCT	TGGTCT	GAGAC	AGTGT	CCTC	AGGT	TAC	AGAG	CAGAG	GATGC	9212
Qy	3505	TGCC	CAGC	AGTGA	TGTTG	CCCTG	AATG	CAC	ACCA	AGGG	CCCC	ACCTG	3564
Db	9213	TGCC	CAGC	AGTGA	TGTTG	CCCTG	AATG	CAC	ACCA	AGGG	CCCC	ACCTG	9272
Qy	3565	TAGG	ACTCC	ACAG	AGTCT	GGCCT	CAC	CTCC	CTACT	GTCA	GTCT	GTAAT	3624
Db	9273	TAGG	ACTCC	AAAG	AGTCT	GGCCT	CAC	CTCC	TACC	ATCA	ATCT	GCAGA	9332
Qy	3625	CTGG	CCGG	CTGT	TACC	CTGA	-GT	ACC	CTCT	CACT	TCTC	CTTC	3683
Db	9333	CTGG	CCGG	CTAT	TACC	CTG	AGGT	GTCT	CTCA	CTTCT	CCTC	CTTC	9392
Qy	3684	CCA	ACC	CAG	AGG	CAGG	ATTCC	CTG	GAGG	CCAC	AGAG	GACCA	3743
Db	9393	CCA	ACCG	-G	AGG	ACAG	GATTCC	CTG	GAGG	CCAC	AGAG	GACCA	9451
Qy	3744	AGTA	GGCCT	TTGTT	AGAG	TCTCC	AAG	TTT	CAG	TTCT	CAG	CTG	3803
Db	9452	AGTA	AGCCT	TTGTT	AGAG	CTCT	AAG	ATT	TGG	TTCT	CAG	CTG	9511
Qy	3804	CTCT	TCTC	CC	CAGG	CTGT	TGGG	TCTT	CATT	TGCC	CAGC	TCTG	3863
Db	9512	CTCT	TCTC	CGT	AGG	CTGT	TGGG	TCCC	ATTG	CCC	CAGC	TTTG	9571
Qy	3864	CCCT	GAC	GAG	ATCAT	GTCT	CTT	GAG	CAG	AGG	AGTCT	GCA	3923
Db	9572	CCCT	GAC	GAG	ATCAT	GTCT	CTT	GAG	CAG	AAG	AGTCT	GCA	9631
Qy	3924	CCCT	TG	AGG	CCCA	ACA	AGG	CCCT	TGGG	CCTG	GTGT	GTGT	3975
Db	9632	GCG	TTG	AGG	CCCA	AGA	AGG	CCCT	TGGG	CCTG	GTGG	TGC	9691
Qy	3976	-----	CTCT	CTCT	CTCT	CTCT	CTCT	CTCT	CTCT	CTCT	CTCT	CTCT	4019
Db	9692	AGC	AGG	AGG	CTGT	CTCT	CTCT	CTCT	CTCT	CTCT	CTCT	CTCT	9751
Qy	4020	CC	ACTG	CTGG	TCA	AC	AGAT	CTCT	CCCC	AGAG	TCTC	AGG	4079
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Qy	4080	CC	ATCA	ACTT	CACT	CG	ACAG	AGG	CAAC	CCAG	TGAG	GGTTC	4139
Db	9812	CC	ATC	AGC	TTCA	CTTG	CTGG	AGG	CAAC	CAAT	TGAG	GGTTC	9871
Qy	4140	GG	CA	AG	CAC	CTCT	TGT	ATC	CTTG	AGT	CTCT	TGTT	4199
Db	9872	GG	CA	AG	CAC	CTCG	CTG	AC	G	CAG	AGT	CTCT	9931
Qy	4200	CT	GATT	TGG	TTGG	TTTT	CTG	CTC	CA	AAT	ATC	GAG	4259
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Db	9992	 AAATGCTGGAGAGAGTCATCAAAAATTACAAGCGTGCTTTCCTGTGATCTTCGGCAAAG	10051
Qy	4320	CCTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCCACCGGCC	4379
Db	10052	 CCTCCGAGTCCCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCCGCCAGCA	10111
Qy	4380	ACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATC	4439
Db	10112	 ACACCTACACCCTTGTCACCTGCCTGGGCCTTTCCTATGATGGCCTGCTGGGTAAATAATC	10171
Qy	4440	AGATCATGCCCAAGACAGGCTTCTTGATAATTGTCTGGTCATGATTGCAATGGAGGGCG	4499
Db	10172	 AGATCTTTCCCAAGACAGGCCTTCTTGATAATCGTCTGGGCACAATTGCAATGGAGGGCG	10231
Qy	4500	GCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGA	4559
Db	10232	 ACAGCGCCTCTGAGGAGGAAATCTGGGAGGAGCTGGGTGTGATGGGGGTGTATGATGGGA	10291
Qy	4560	GGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAA	4619
Db	10292	 GGGAGCACACTGTCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAA	10351
Qy	4620	AGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGG	4678
Db	10352	 ACTACCTGGAGTACCGGCAGGTACCGGCAGTAATCCTGCGCGCTATGAGTTCCTGTGGG	10411
Qy	4679	GTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCA	4738
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Qy	4739	GTGCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAG	4798
Db	10472	 ATGCAAGAGTTCGCATTGCCTACCCATCCCTGCGTGAAGCAGCTTTGTTAGAGGAGGAAG	10531
Qy	4799	AGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGG----GGACTGGGCCAGTG	4854
Db	10532	 AGGGAGTCTGAGCATGAGTTGCAGCCAGGGCTGTGGGGAAGGGGCAGGGCTGGGCCAGTG	10591
Qy	4855	CACCTTCCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCCATTCCT	4914
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Qy	4915	CAC TC----TGAAGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGA	4970
Db	10650	 CACTCTGTTTGAAGAAAATAGTCAGTGTTCTTAGTAGTGGGTTTCTATTTTGTGGATGA	10709
Qy	4971	CTTGGAGATTTATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTAAAGGGATGG	5030
Db	10710	 CTTGGAGATTTATCTCTGTTTCCTTTTACAATTGTTGAAATG-TTCCTTTTAAATGGATGG	10768
Qy	5031	TTGAATGAAC TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATAT	5090
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Qy	5091	AGTTTAAAGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAA	5150
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Db 10889 TTTGGGACATAATAACAGCAGTGGAGTAAGTATTTAGAAGTGTG---AATTCACCGTGAA 10945

Qy 5208 ATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAG 5267  
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Db 10946 ATAGGTGAGAT-----AAATTAAGATACTTAATCCCGCCTTATGCCTCAG 10993

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Db 11051 ATGTAAGAGAAATTAATCTGAATAAATAATTCTTTCTGTTAACTGGCTCATTTCTTCTC 11110

Qy 5388 CATGCACTGAGCATCTGCTTTTTGGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAA 5447  
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Db 11111 TATGCACTGAGCATCTGCTCTGTGGAAGGCCAGGATTAGTAGTGAGATACTAGGGTAA 11170

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# RESULT 14

HSU10687

LOCUS HSU10687 11495 bp DNA linear PRI 23-JUN-1995

DEFINITION Human MAGE-4a antigen (MAGE4a) gene, complete cds.

ACCESSION U10687

VERSION U10687.1 GI:533514

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 11495)

AUTHORS De Plaen,E., Arden,K., Traversari,C., Gaforio,J.J., Szikora,J.P.,  
 De Smet,C., Brasseur,F., van der Bruggen,P., Lethe,B.,  
 Lurquin,C.Brasseur.R., Chomez,P., De Backer,O., Cavenee,W. and  
 Boon,T.

TITLE Structure, chromosomal localization, and expression of 12 genes of  
 the MAGE family

JOURNAL Immunogenetics 40 (5), 360-369 (1994)

PUBMED 7927540

REFERENCE 2 (bases 1 to 11495)

AUTHORS De Plaen,E.

TITLE Direct Submission

JOURNAL Submitted (14-JUN-1994) Etienne De Plaen, Ludwig Institute for  
 Cancer Research, 74 Avenue Hippocrate, Brussels, 1200, Belgium

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FEATURES                      Location/Qualifiers
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ORIGIN

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Query Match          46.8%;  Score 2655;  DB 5;  Length 11495;
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Qy      21 CCTCCCCCTACCAACCCCAATCCCTCCCTTTACGCCACCCATCCAAACATCTTCACGCTC 80
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Qy      81 ACCCCCAGCCCCAAGCCAGGCAGAAATCCGGTTCCACCCCTGCTCTCAACCCAGGGAAGC-C 139
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Db	6528		6587
Qy	1146	ATTCCCCACCTGTGCCCTATCTCCCCAACCCCCAACCCAGCCTCATACCCCCCTCCCC	6587
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Db	6588		6647
Qy	1266	CACCCCTACCTTCATCCCCATCAGTGCAGCATCCGGTTCACCCCTGCTTTCAATCCAGG	6647
Qy	1326	AAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGAGAAGC	785
Db	6648		6707
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Qy	1086	GCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCCCCAAG	1145
Db	6977	GCCCAGGCCCTGCCAGGAATCAAAGTCAGAAACC-TGAGAGGGAAGTGGAGTCCCCCAAG	7035
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Db	7405	GCCACTAAAGCTACAGGGGACTCTAGAGTCAAGAGCTTGGTGTGCCCA-----	7452
Qy	1745	AGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGGACCC	1804
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Qy	1985	CTGATGGAGGGAAGGGG-----CTTGAACAGGGCCTCAGGGGAGCAGAGGGAG-----	2032
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Qy	2141	GGGACTCAGATTGCAT--GGGGGTGGGACCAGGCCTGCAAGGCTTACGCGGAGGAAGAG	2198
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Qy	2199	GAGGGAGGACTCAGGGGACCTTGG AATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTC	2258
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Qy	2315	AGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTCAACAGAGGGAGGAGTTCAGGATCCAT	2374
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Qy	2375	ATGGCCCAAGATGTGCC-CCCTTCATGAGGACTGGGGATATCCCCGGCTCAGAAAAGAGG	2433
Db	8077	AGGACCCAAGGTGTGCCACACTTCAGGGAATGGGGATACCTGTGGCTCAGAAAGACGG	8136
Qy	2434	GACTCCACACAGTCTGGCTGTCCCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGG	2493
Db	8137	GACCCACAGAGTCTGGCTGTCCCTGTCTTAGCTCAGGGGGGACCAGAGGAGGGATGG	8196
Qy	2494	CGGTATGTTCCATTCTCACTTGTACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATG	2553
Db	8197	CCCTATGTGCCAATTTCACTTGTTCACAGGCAGGAAGTTGGGGAACCTTCAGGGAGATG	8256
Qy	2554	GGGTCTTGGGGTAAAGGGGGGATGTCTACTCATGTCAGGGAATTGGGGGTTGAGGAAGCA	2613
Db	8257	AGGTTTTTGAGTAAAGGGGCAATGTTTGCTCATCTCAGGGGGTTGGGGGTTGAGGAAGGG	8316
Qy	2614	CAGGCGCTGGCAGGAATAAAGATGAGTGAGACAGACAAGGCTATTGGAATCCACACCCCA	2673
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Db	8317	CAGGCCCTGTCAGGAGCAAACATGAGT-ACCCACAGGAGGCCATCAGAACCTCACCCCA	8375
Qy	2674	GAACCAAGGGGTGACCCCTGGACACCTCACCCAG-----GATGTGGCTTCTTTTTC	2725
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Qy	2966	GTCCTTCCGTTATCCTGGGATCATTGATGTCAGGGACGGGGAGGCCTTGGTCTGAGAAGG	3025
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RESULT 15

U82696

LOCUS U82696 161664 bp DNA linear PRI 31-DEC-2002

DEFINITION Homo sapiens chromosome X clone ICRFXc104-F064, ICRFXc104-G0799, Qc-14E2, Qc-13D8, Qc-7G11, ICRFXc104-E0681, Qc-11C8, Qc-9A9 map q28, complete sequence.

ACCESSION U82696

VERSION U82696.2 GI:27436770

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 161664)

AUTHORS Galgoczy, P., Wen, G. and Platzter, M.

TITLE Chromosome X genomic sequence

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 161664)

AUTHORS Gloeckner, G., Rosenthal, A., Drescher, B., Schattevoy, R., Hinzmann, B. and Poustka, A.

TITLE Direct Submission

JOURNAL Submitted (19-DEC-1996) Genome Analysis, Institut for Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany

REFERENCE 3 (bases 1 to 161664)

AUTHORS Platzter, M.

TITLE Direct Submission

JOURNAL Submitted (31-DEC-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany

COMMENT On Dec 31, 2002 this sequence version replaced gi:2735037.

----- Genome Center

Center: Insitute of Molecular Biotechnology

Center code: IMB

Web site: <http://genome.imb-jena.de/>

Contact: [gscj-submit@genome.imb-jena.de](mailto:gscj-submit@genome.imb-jena.de)

----- Project Information

Center project name: x81+

Center clone name: ICRFXc104-F064 to Qc-9A9

----- Summary Statistics

Sequencing vector: M13 and pUC18; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 161664 bases at least Q40

Consensus quality: 161664 bases at least Q30

Consensus quality: 161664 bases at least Q20

Quality coverage: 26.71x

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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone.

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 Neighboring sequence information:

This clone is overlapped by RP11-366F6, RP1-228J9, RP1-77B24, RP1-73F14.

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 Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

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Qy      4915 CACTC-----TGAAGAGAGCGGTCAGTGTTCAGTAGTAGGTTCTGTTCTATTGGGTGA 4970
        |||||      ||||| |  ||||| ||||| ||||| || ||||| |||
Db      64910 CACTCTGTTTGAAGAAAATAGTCAGTGTTCCTTAGTAGTGGGTTCTATTTTGTGGATGA 64969

Qy      4971 CTTGGAGATTTATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGG 5030
        ||||| ||||| ||||| ||||| ||||| ||||| || ||||| |||||
Db      64970 CTTGGAGATTTATCTCTGTTTCCTTTTACAATTGTTGAAATG-TTCCTTTTAATGGATGG 65028

Qy      5031 TTGAATGAACCTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATAT 5090
        ||||| ||||| ||||| ||||| ||||| ||||| || ||||| |||||
Db      65029 TTGAATTAACCTCAGCATCCAAGTTTATGAATCGTAGTTAACGTATATTGCTGTTAATAT 65088

Qy      5091 AGTTTAAGGGTAAGAGTCTTGTTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAA 5150
        ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      65089 AGTTTAGGAGTAAGAGTCTTGTTTTTTTATTTCAGATTGGGAAATCCGTTCTATTTTGTGAA 65148

Qy      5151 TTGGG---ATAATAACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAA 5207
        || || ||||| ||||| ||||| ||||| ||||| ||||| || |||||
Db      65149 TTTGGGACATAATAACAGCAGTGGAGTAAGTATTTAGAAAGTGTG---AATTCACCGTGAA 65205

Qy      5208 ATAGATGAGATAAAGAAGCTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAG 5267
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      65206 ATAGGTGAGAT-----AAATTAAAAGATACTTAATCCCGCCTTATGCCTCAG 65253

Qy      5268 TCTATTCTGTAAAATTT-TTAAAGATATATGCATACCTGGATTTCCTTGCCCTTCTTTGAG 5326
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      65254 TCTATTCTGTAAAATTTAAAAAATATATATGCATACCTGGATTTCCTTGCCCTC---GTG 65310

Qy      5327 AATGTAAGAGAAATTAAATCTGAATAAAGAATTCTTCCTGTTCAGTGGCTCTTTTCTTCT 5386
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      65311 AATGTAAGAGAAATTAAATCTGAATAAATAATTCTTCTGTAACTGGCTCATTCTTCTCT 65370

Qy      5387 CCATGCACTGAGCATCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTA 5446
        | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      65371 CTATGCACTGAGCATCTGCTCTGTGGAAGGCCCAGGATTAGTAGTGGAGATACTAGGGTA 65430

Qy      5447 AGCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGA 5506
        ||||| || |||| ||||| ||||| || ||||| ||||| ||||| |||||
Db      65431 AGCCAGACACACACCTACCGATAGGGTATTAAGAGTCTAGGAGCGCGGTCATATAATTAA 65490

Qy      5507 GGTGGCAAGATGTCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGC 5566
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      65491 GGTGACAAGATGTCTCTAAGATGTAGGGGAAAAGT----AACGAGTGTGGGTATGGGGC 65546

Qy      5567 TCCGGGTGAGAGTGGTGGAGTGTCATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAAA 5626
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      65547 TCCAGGTGAGAGTGGTCGGGTGTAAATTCCTGTG-TGGGGCCTTTGGGCTTTGGGAAA 65605

Qy      5627 CTGCAGTTCCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
        || || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      65606 CTCCATTTTCTTCTGAGGGATCTGATTCTAATGAAGCTTGGTGGGTCC 65653

```

Search completed: August 25, 2006, 18:36:48  
Job time : 30927 secs

SCORE 1.3 BuildDate: 12/06/2005
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# SCORE Search Results Details for Application 08819669 and Search Result us-08-819-669e- 8.rng.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

This page gives you Search Results detail for the Application 08819669 and Search Result us-08-819-669e-8.rng.

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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2006, 08:55:59 ; Search time 3165 Seconds  
(without alignments)  
12499.380 Million cell updates/sec

Title: US-08-819-669E-8  
Perfect score: 5674  
Sequence: 1 CCCGGGGCACCCTGGCATC.....TAATGATCTTGGGTGGATCC 5674

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*  
15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	5674	100.0	5674	2	AAQ72477	Aaq72477 Tumour re
2	5674	100.0	5674	2	AAX84113	Aax84113 MAGE-1 ge
3	5672.4	99.9	5674	2	AAQ32352	Aaq32352 MAGE-1 nu
4	5650.8	99.6	5724	2	AAQ98902	Aaq98902 Tumour re
5	2655	46.8	11495	2	ABQ76203	Abq76203 Human tum
6	2513.6	44.3	4895	2	ABQ76204	Abq76204 Human tum
7	2513.6	44.3	4895	7	ADS73099	Ads73099 Human kid
8	2513.6	44.3	4895	7	ADW41953	Adw41953 cDNA elev
9	2429.6	42.8	4736	2	ABQ76206	Abq76206 Human tum
10	2422.8	42.7	4741	2	ABQ76205	Abq76205 Human tum
11	2419	42.6	2419	2	AAQ32351	Aaq32351 Antigen E
12	2419	42.6	2419	2	AAQ72476	Aaq72476 Tumour re
13	2419	42.6	2419	2	AAX84112	Aax84112 Antigen E
14	2415.8	42.6	2419	2	AAT05086	Aat05086 MZ2-MEL a
15	2408	42.4	2420	2	AAQ72472	Aaq72472 Tumour re
16	2408	42.4	2420	2	AAQ85435	Aaq85435 Human mel
17	2408	42.4	2420	2	ABQ76198	Abq76198 Human tum
18	2408	42.4	2420	8	ABQ83847	Abq83847 Human MAG
19	2408	42.4	2420	10	ADC09583	Adc09583 MAGE-1 DN
20	2408	42.4	2420	12	ADM72822	Adm72822 Human MAG
21	2408	42.4	2420	12	ADQ36554	Adq36554 Human MAG
22	2408	42.4	2420	13	ADT93875	Adt93875 Non-small
23	2408	42.4	2420	14	ADW44360	Adw44360 Human mel
24	2408	42.4	2420	15	AEF02866	Aef02866 Wild-type
25	2408	42.4	2420	15	AEF13905	Aef13905 Human MAG
26	2404.8	42.4	2420	9	ACD42236	Acd42236 Human MAG
27	2404.8	42.4	2420	9	ACH04045	Ach04045 Human cDN
28	2400.6	42.3	2418	2	AAX84103	Aax84103 E antigen
c 29	2307.6	40.7	302250	6	ABL67703	Abl67703 Oesophagu
30	2306	40.6	302250	6	ABL67703	Abl67703 Oesophagu
31	2117.8	37.3	4559	2	ABQ76199	Abq76199 Human tum
32	2117.8	37.3	4559	8	ABQ83848	Abq83848 Human MAG
33	2117.8	37.3	4559	10	ADC09584	Adc09584 MAGE-2 DN
34	2117.8	37.3	4559	12	ADM72823	Adm72823 Human MAG
35	2058.8	36.3	4157	2	AAQ72478	Aaq72478 Tumour re
36	2058.8	36.3	4157	2	AAX84114	Aax84114 MAGE-2 ge
37	2057.2	36.3	4157	2	AAQ32353	Aaq32353 MAGE-2 ge
38	1945	34.3	4523	4	AAD06131	Aad06131 Human MAG
39	1945	34.3	4523	12	ADO23388	Ado23388 DNA encod
40	1932	34.1	2014	8	ABX95024	Abx95024 DNA encod
41	1765.8	31.1	4204	4	AAS02056	Aas02056 DNA encod
42	1765.8	31.1	4204	9	ACH04024	Ach04024 Human cDN
43	1762.6	31.1	4204	2	ABQ76200	Abq76200 Human tum
44	1762.6	31.1	4204	2	AAX26974	Aax26974 cDNA enco
45	1762.6	31.1	4204	3	AAA37927	Aaa37927 Human MAG

#### ALIGNMENTS

RESULT 1  
AAQ72477



```

ID      AAQ72477 standard; DNA; 5674 BP.
XX
AC      AAQ72477;
XX
DT      25-MAR-2003 (revised)
DT      22-JUN-1995 (first entry)
XX
DE      Tumour rejection antigen MAGE-1 encoding DNA.
XX
KW      Tumour rejection antigen; melanoma antigen-1; MAGE-1; MAGE-3; cancer;
KW      cytolytic T cells; antigen D; human leucocyte antigen; ss.
XX
OS      Homo sapiens.
XX
FH      Key          Location/Qualifiers
FT      CDS          3881..4711
FT                      /*tag= a
XX
PN      WO9423031-A1.
XX
PD      13-OCT-1994.
XX
PF      17-MAR-1994; 94WO-US002877.
XX
PR      26-MAR-1993; 93US-00037230.
XX
PA      (LUDW-) LUDWIG INST CANCER RES.
XX
PI      Gaugler B, Van Den Eynde B, Boon-Falleur T, Van Der Bruggen P;
XX
DR      WPI; 1994-333192/41.
XX
PT      New tumour rejection antigen precursor MAGE3 - useful in treatment and
PT      diagnosis of cancer.
XX
PS      Example 26; Page 59; 105pp; English.
XX
CC      AAQ72477 is the DNA sequence which encodes melanoma antigen-1 (MAGE-1).
CC      Another melanoma antigen MAGE-3 is encoded by AAQ72470, this is a tumour
CC      rejection antigen precursor. Melanomas characterised by the expression of
CC      MAGE-3 can be detected, or monitored, by contacting a test sample with an
CC      agent that can recognise MAGE-3. The melanoma can be treated by the
CC      administration of cytolytic T cells specific for the complex of antigen D
CC      (the mature rejection antigen derived from MAGE-3) and a human leucocyte
CC      antigen (esp. HLA-A1). (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ      Sequence 5674 BP; 1276 A; 1644 C; 1569 G; 1185 T; 0 U; 0 Other;

Query Match          100.0%; Score 5674; DB 2; Length 5674;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCCGGGGCACCACCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
        |||
Db      1 CCCGGGGCACCACCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy      61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
        |||
Db      61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy      121 CTCTCAACCCAGGGAAGCCCGAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

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Db	121		CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG	180
Qy	181		TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Db	181		TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Qy	241		CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Db	241		CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Qy	301		AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Db	301		AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Qy	361		TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Db	361		TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Qy	421		CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Db	421		CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Qy	481		CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Db	481		CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Qy	541		CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Db	541		CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Qy	601		CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Db	601		CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Qy	661		CACCCCCACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCC	720
Db	661		CACCCCCACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCC	720
Qy	721		CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATGTGGGGCAGAGA	780
Db	721		CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATGTGGGGCAGAGA	780
Qy	781		GAAGCGAGGTTTCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781		GAAGCGAGGTTTCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841		CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Db	841		CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Qy	901		GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901		GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961		CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961		CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021		TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080

Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCC TGGACCACCCGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCC TGGACCACCCGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980

Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTGAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTGAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880

Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTACCCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTACCCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCC TTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCC TTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Db	3181	GTCCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTC	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTC	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCTGAGTACCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCTGAGTACCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTAGTTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTAGTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840

Db	3781	 AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	 CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	 TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCCTCCTCCTGCTGCTGGGCACCTTGAGGAGGTGCC	4020
Db	3961	 TGTGCAGGCTGCCACCTCCTCCTCCTCCTCCTGCTGCTGGGCACCTTGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	 CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	 CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	 GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	 TGATTTGGTTGGTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	 AATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	 CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTGATAATCA	4440
Db	4381	 CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	 GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	 CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCATATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	 GGAGCACAGTGCCATATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621	 GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740

Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA	5220
Qy	5221	AGAAGTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAAGTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCTGTTCAGTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCTGTTCAGTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTTTGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Db	5401	TCTGCTTTTTTGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Qy	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Db	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Qy	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Db	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Qy	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTGGGAACTGCAGTTCCCTTCT	5640
Db	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTGGGAACTGCAGTTCCCTTCT	5640

Qy 5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674  
 |||||  
 Db 5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

RESULT 2

AAX84113

ID AAX84113 standard; DNA; 5674 BP.

XX

AC AAX84113;

XX

DT 08-SEP-1999 (first entry)

XX

DE MAGE-1 gene.

XX

KW Tumour rejection antigen; vaccine; cancer; MAGE-1 gene; ss.

XX

OS Homo sapiens.

XX

PN US5925729-A.

XX

PD 20-JUL-1999.

XX

PF 02-MAY-1994; 94US-00142368.

XX

PR 23-MAY-1991; 91US-00705702.

PR 09-JUL-1991; 91US-00728838.

PR 23-SEP-1991; 91US-00764365.

PR 12-DEC-1991; 91US-00807043.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Van Der Bruggen P, Traversari C, Lurquin C, Boon T, De Plaen E;

PI Van Pel A, Chomez P, Van Den Eynde B;

XX

DR WPI; 1999-418294/35.

XX

PT New tumour rejection antigen is useful as a vaccine against cancerous diseases.

XX

PS Disclosure; Col 39-46; 58pp; English.

XX

CC This sequence represents the MAGE-1 gene sequence. The invention relates to a tumour rejection antigen sequence that is useful as a tumour rejection antigen for vaccination against cancerous conditions

XX

SQ Sequence 5674 BP; 1276 A; 1644 C; 1569 G; 1185 T; 0 U; 0 Other;

Query Match 100.0%; Score 5674; DB 2; Length 5674;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60  
 |||||  
 Db 1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy 61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120  
 |||||  
 Db 61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120



Qy	121	CTCTCAACCCAGGGAAGCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG	180
Db	121	CTCTCAACCCAGGGAAGCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG	180
Qy	181	TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Db	181	TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Qy	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Db	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Qy	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Db	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Qy	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Db	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Qy	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Db	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Qy	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Db	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Qy	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Db	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Qy	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCATCCGCCAGCCATTCCACCCT	660
Db	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCATCCGCCAGCCATTCCACCCT	660
Qy	661	CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Db	661	CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Qy	721	CCAGGAAACATCCGGGTGCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721	CCAGGAAACATCCGGGTGCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080

Db	1021		TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081		GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081		GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141		CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141		CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201		CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201		CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261		ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261		ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321		CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321		CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381		GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381		GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441		TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441		TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501		ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501		ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561		ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561		ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621		CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621		CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681		CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681		CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741		GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741		GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801		ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801		ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861		CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861		CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921		TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980

Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGTCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGTCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTGAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTGAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880

Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Db	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780

Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTTGGGCACCTTGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTTGGGCACCTTGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCTCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATCTCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCATATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCATATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740

Db	4681		CCAAGGGCCCTCGCTGAAACCAAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741		GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741		GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801		GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801		GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861		CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
Db	4861		CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
Qy	4921		GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921		GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981		TATCTTTGTTCTCTTTTGAATGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981		TATCTTTGTTCTCTTTTGAATGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041		TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTCTGTGTATATAGTTTAAGGG	5100
Db	5041		TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTCTGTGTATATAGTTTAAGGG	5100
Qy	5101		TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101		TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161		AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Db	5161		AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Qy	5221		AGAATAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Db	5221		AGAATAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281		ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281		ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341		TAAATCTGAATAAAGAATTCTTCTGTTCAGTGGCTCTTTCTTCTCCATGCACTGAGCA	5400
Db	5341		TAAATCTGAATAAAGAATTCTTCTGTTCAGTGGCTCTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401		TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATA	5460
Db	5401		TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATA	5460
Qy	5461		CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Db	5461		CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Qy	5521		CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Db	5521		CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Qy	5581		GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT	5640

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Db      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
Qy      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
        |||||
Db      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

```

RESULT 3

AAQ32352

ID AAQ32352 standard; DNA; 5674 BP.

XX

AC AAQ32352;

XX

DT 25-MAR-2003 (revised)

DT 22-APR-1993 (first entry)

XX

DE MAGE-1 nucleic acid.

XX

KW melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;

KW tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 3881..4711

FT /\*tag= a

XX

PN WO9220356-A1.

XX

PD 26-NOV-1992.

XX

PF 22-MAY-1992; 92WO-US004354.

XX

PR 23-MAY-1991; 91US-00705702.

PR 09-JUL-1991; 91US-00728838.

PR 23-SEP-1991; 91US-00764364.

PR 12-DEC-1991; 91US-00807043.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Boon T, Van Der Bruggen P, Van Den Eynde B, Van Pel A, De Plaen E;

PI Lurquin C, Chomez P, Traversari C;

XX

DR WPI; 1992-415460/50.

XX

PT Nucleic acid mol. encoding a human tumour rejection antigen precursor -

PT useful as an immunostimulant in a vaccine for treating and preventing

PT cancers, also useful in diagnosis.

XX

PS Disclosure; Page 71-73; 142pp; English.

XX

CC The sequences given in AAQ32352-69 represent a new family of genes  
 CC referred to as melanoma antigens (MAGE). The cDNAs of this gene family  
 CC were identified during the isolation of the antigen E gene. The MAGE  
 CC cDNAs, when tested, did not transfer expression of antigen E, but they  
 CC did show substantial homology to the antigen E cDNA sequence. The MAGE  
 CC DNAs share a certain degree of homology with each other and are expressed  
 CC in tumour cells including several types of human tumor cells as well as  
 CC in human tumors. MAGE expression is not restricted to melanomas. MAGE  
 CC refers to a family of tumor rejection antigen precursors. The antigens  
 CC resulting from these genes are referred to as MAGE TRAs or melanoma

CC antigen tumor rejection antigens. See also AAQ32351. (Updated on 25-MAR-  
CC 2003 to correct PN field.)

XX

SQ Sequence 5674 BP; 1277 A; 1644 C; 1568 G; 1185 T; 0 U; 0 Other;

Query Match 99.9%; Score 5672.4; DB 2; Length 5674;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5673; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
      |||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
      |||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
      |||
Db    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
      |||
Db    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
      |||
Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
      |||
Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
      |||
Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480
      |||
Db    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

Qy    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540
      |||
Db    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540

Qy    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCTATCCAACCCCCA 600
      |||
Db    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCTATCCAACCCCCA 600

Qy    601 CCCCACATCCCCCACCCATCCCTCAACCTGATGCCCATCCGCCAGCCATTCCACCCT 660
      |||
Db    601 CCCCACATCCCCCACCCATCCCTCAACCTGATGCCCATCCGCCAGCCATTCCACCCT 660

Qy    661 CACCCCCACCCCCACCCCCACGCCCCTCCACCCCCACCCAGGCAGGATCCGGTTCCCG 720
      |||
Db    661 CACCCCCACCCCCACCCCCACGCCCCTCCACCCCCACCCAGGCAGGATCCGGTTCCCG 720

Qy    721 CCAGGAAACATCCGGGTGCCGGATGTGACGCCACTGACTTGCGCATTTGTGGGGCAGAGA 780
      |||
Db    721 CCAGGAAACATCCGGGTGCCGGATGTGACGCCACTGACTTGCGCATTTGTGGGGCAGAGA 780
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Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTATTTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTATTTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGTTTATAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGTTTATAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740

Db	1681		1740
Qy	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCAGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCAGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGTCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGTCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640

Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTCAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTCAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGATTCTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGATTCTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCTGAGGGCCCGTGGAATTCCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCTGAGGGCCCGTGGAATTCCT	3420
Qy	3421	CTTCTGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCTGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540

Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACCTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACCTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTATCAAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTATCAAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440

Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAACTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCCGTTCAGTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400

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Db      5341  |||||TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400
Qy      5401  TCTGCTTTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
Db      5401  |||||TCTGCTTTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
Qy      5461  CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Db      5461  |||||CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Qy      5521  CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Db      5521  |||||CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Qy      5581  GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT 5640
Db      5581  |||||GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT 5640
Qy      5641  GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
Db      5641  |||||GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

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#### RESULT 4

AAQ98902

ID AAQ98902 standard; DNA; 5724 BP.

XX

AC AAQ98902;

XX

DT 28-FEB-1996 (first entry)

XX

DE Tumour rejection antigen (MAGE-1) gene.

XX

KW Tumour rejection antigen; MAGE-1; monoclonal antibody; MAb; diagnosis;

KW immunoassay; cancer; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 3881..4711

FT /\*tag= a

FT /product= "Tumour rejection antigen MAGE-1."

FT /note= "The CDS is not indicated in the text of the  
specification but is suggested in the layout of the  
sequence."

XX

PN W09520974-A1.

XX

PD 10-AUG-1995.

XX

PF 05-JAN-1995; 95WO-US000095.

XX

PR 01-FEB-1994; 94US-00190411.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

PA (SLOK ) MEMORIAL SLOAN-KETTERING CANCER CENT.

XX

PI Chen Y, Stockert E, Chen Y, Garin-Chesa P, Rettig WJ;

PI Van Der Bruggen P, Boon-Falleur T, Old LJ;

XX

XX

XX

XX

XX

Sequence 5724 BP; 1282 A; 1653 C; 1589 G; 1200 T; 0 U; 0 Other;

Query Match 99.6%; Score 5650.8; DB 2; Length 5724;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5652; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCGGGGCACCACCTGGCATCCCTCCCCCTACCACCCCCAATCCCTCCCTTTACGCCACCC 60

Db 1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy 61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Db 61 ATCCAAACATCTTCACGCTACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCACCCCTG 120

Qy 121 CTCTCAACCCAGGGAAGCCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Db 121 CTCTCAACCCAGGGAAGCCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy 181 TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Db 181 TTAGAGAGAAGCGAGGTTTTCTGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy 241 CCCAGCTCTGTAAGGAGGCCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Db 241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy            301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCTGGACCATCTGGTGGTGGACTTC    360  
             | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy 361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Db 361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy 421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

Db 421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

Qy 481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCAAC 540

Db 481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540

Qy 541 CCCCAC TCCAAT GCTCA CTCCCG TGACCA ACCCC CTTCAT TGTCAT TCCAAC CCCCCA 600

Db	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCAATTCCAACCCCCA	600
Qy	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT	660
Db	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT	660
Qy	661	CACCCCCACCCCAACCCACGCCCCACTCCACCCCAACCAGGCAGGATCCGGTTCCCG	720
Db	661	CACCCCCACCCCAACCCACGCCCCACTCCACCCCAACCAGGCAGGATCCGGTTCCCG	720
Qy	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGGCCC	1140
Qy	1141	CCAAGACTGCAC'TCCAATCCCCACTCCCACCCATTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141	CCAAGACTGCAC'TCCAATCCCCACTCCCACCCATTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCCTCACTGCCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCCTCACTGCCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500



Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCTAGGACACCGACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCTAGGACACCGACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400

Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTCAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTCAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCCTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCCTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTTGGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCTCCTG	3360

Db	3301	CAGAGGGGTCATCCACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCGTGGATTCTCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCGTGGATTCTCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTCCCCTACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTCCCCTACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260

Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTCAATCAAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTCAATCAAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160

Qy	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCAGTCTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCAGTCTGAGCA	5400
Qy	5401	TCTGCTTTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Db	5401	TCTGCTTTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Qy	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Db	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Qy	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Db	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Qy	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT	5640
Db	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT	5640
Qy	5641	GGGGGAGCTGATTG	5654
Db	5641	GGGGGAGCTGGCTG	5654

# RESULT 5

ABQ76203

ID ABQ76203 standard; DNA; 11495 BP.

XX

AC ABQ76203;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human tumour antigen MAGE-4a DNA.

XX

KW Tumour antigen; human; vaccine; cellular immune response; immunogen;  
cancer; tumour; MAGE-4a; ds.

XX

OS Homo sapiens.

XX

PN US6287569-B1.

XX

PD 11-SEP-2001.

XX

PF 06-APR-1998; 98US-00056105.

XX

PR 10-APR-1997; 97US-0043467P.

XX

http://es/ScoreAccessWeb/GetItem.action?AppId=08819669&seqId=609517&ItemName=us... 8/30/06

Qy	427	GTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACATCATGCT	486
Db	6389	GTGATCAGTGCAGGACTGGTGGGGGT-----AGGCTCTGCCAGGCATCAACGT	6436
Qy	487	CAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCCTCCCGTGACCAACCCCCAC	546
Db	6437	CAGGACCCTAGGAGAGGGCTGAGTGTCCCCA---CCCCATTCTATCCCTTACCCCTT	6493
Qy	547	TCCAATGCTCACTCCCGTGACCAACCCCCCTCTTCATTGTCTATTCCAACCCCCACCCCAC	606
Db	6494	TCCCATCTGCACTCCC-----TACCCATCTGTACCCCC	6527
Qy	607	ATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCTCACCCC	666
Db	6528	ATTCCCCACCTGTGCCCTATCTCCCCAACCCCCCAACCAGCCTCATACCCCCCTCCCC	6587
Qy	667	CACCCCCACCCACGCCCCACTCCCACCCCCACCCAGGCAGGATCCG-GTTCCCGCCAGG	725
Db	6588	CACCCCTACCTTCATCCCCATCAGTGCAGCATCCGGTTCCACCCCTGCTTTCAATCCAGG	6647
Qy	726	AAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGAGAAGC	785
Db	6648	CAAGCCCTGGGTGGCCGGATGTGATGCCACTGACTTGTGAATTGAGGGTTAGAGAGAAGT	6707
Qy	786	GAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGGCTCTG	845
Db	6708	GAGTTTCTGGGTCTGAAGGGTGGC-TTGAGATCGGCAGAGGGAAGGTGGCCCAGGCTTTG	6766
Qy	846	TGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCCGCCACTCCAAATAGAGAG	905
Db	6767	TGAAGAGGCAAAGTGAGACTCTGAGGGAGGATTCAGGAAACCCCTATCCCTGATAGAGGG	6826
Qy	906	CCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCCACCGCGGGAAGACGTCT	965
Db	6827	TCCCAGCCCTGGACTACCC-----CGCGGAGGCTGACTTCT	6862
Qy	966	CAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTCTTCTC	1025
Db	6863	CAGACTGGGCTGCTCCCCACCTCCGCCCC-----TTCGCAACGCGTTTGTTTAAGCCAC	6917
Qy	1026	CCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGGGCAGG	1085
Db	6918	AGGGGACTCTGGAGTCAGAGGTTGGTGTGATCAGGGAAGGGCTGGTTAGGAGA-GGCATG	6976
Qy	1086	GCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCCCCAAG	1145
Db	6977	GCCCAGGCCCTGCCAGGAATCAAAGTCAGAAACC-TGAGAGGGAAGTCCCTCCCCAAG	7035
Qy	1146	ACTGCACTCCAATCCCCACTCCCACCCATTTCGCTATCCCATTCCCCACCCAACCCCCAT	1205
Db	7036	ATCCTAGTCTAACCCCCACTCCCACAA-----	7062
Qy	1206	CTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACCACCT	1265
Db	7063	-----ATCCGCTGCCATTTGCTGCTCCATTTCCCATTCCTTGCCCT	7104
Qy	1266	CCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAACCCAC	1325
Db	7105	CCACCCTACCA-----	7116
Qy	1326	CCTCATCTCTCTCATGTGCCCCACTCCCATCGCTCCCCCATCTGGCAGAATCCGGTTT	1385

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                                ||||| |||
Db      7117 -----GGCAGAATCCAGTTC 7131

Qy      1386 GCC-CCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACTTGAA 1444
        || |||| |||| ||||| ||| | | | | |
Db      7132 CCCTTCTGCTATCAATCCAGGGAACCCAGGCTTGGTGCTGGGATGTTTTT----- 7183

Qy      1445 CCTCACAGATCTGAGAGAAGCCAGGTTCAATTTAATGGTCTGAGGGGCGGCTTGAGATCC 1504
        || | | | | | | | | | | | | | | | |
Db      7184 -----TGGGGGTCAGAGAATCAAGGGCATAGTCTGAGGGGCCAGTTGAGATCG 7232

Qy      1505 ACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGGACTG 1564
        ||||| || | | | | | | | | | | | | | | | |
Db      7233 GCTGAGGGGAGCGGGCCCAAGCTCTGTGGCGAGGCAAGGTGAGACTCTGAGGAAGGACTG 7292

Qy      1565 AGGAGGCACACACCCAGGTAGATGGCCCCAAATGATCCAGTACCACCCCTGCTGCCAG 1624
        ||||| | | |||| | | |||| | | |||| | | ||||| | |
Db      7293 AGGAGGCCCCACCAAGATAGA-GGAACCCAAATAATCCAGCGCAGCTCCTGCTGCCAG 7351

Qy      1625 CCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCCCACT 1684
        ||||| ||||| || ||| |||| | | | | | | |||||
Db      7352 TCCTGGACCACCCGG---GGGAAGACTTCTCA---GGCTAGGCCATCCAGCTCCCACT 7404

Qy      1685 GCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTTGGTC 1744
        ||||| || | ||||| | ||| |||| | ||| |
Db      7405 GCCACTAAAGCTACAGGGGACTCTAGAGTCAAGAGCTTGGTGTGCCCA----- 7452

Qy      1745 AGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGGACCC 1804
        ||||| ||||| || ||| |||| | ||||| |||||
Db      7453 -----AGGCAGGGCCAGGC-----TCTGCCTGGCATCGGGGTCAGGACCT 7493

Qy      1805 TGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACCCAC 1864
        || ||||| ||||| | |||| |||| | || | | ||
Db      7494 TGAGAGGGAAC TGAGGGCGCTACACCCCAACCCATCCGCATTC-----CAACAT 7543

Qy      1865 TCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTGTCAA 1924
        | || |||| | | | || | || || | | |||| ||||
Db      7544 GCCCAGCCCCATCCCCAATCCGTTTTGCAGAATCCATTTT---TCCCCTGCAGTCAA 7599

Qy      1925 CCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCAGGGT 1984
        ||| |||| | ||||| ||||| ||||| ||||| ||||| ||||
Db      7600 CCCCAGGAAGACCTGGGAATGGT---CAGGCACTCGGATCTTGACATCCACATCGAGGGC 7656

Qy      1985 CTGATGGAGGGAAGGGG-----CTTGAACAGGGCCTCAGGGGAGCAGAGGGAG----- 2032
        | | || |||| | ||| || ||||| ||||| ||||| ||||
Db      7657 TGAAGGAGGGAGAGGGTTTGGTATCATGAGCAGAGCCTCAGGGTAGCAGAGGGAGGACCC 7716

Qy      2033 -GGCCCTACTGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCC-----TAGGAC 2082
        ||||| ||| ||||| ||||| ||||| ||||| ||||| |||
Db      7717 TGGCCCTCCTGGGAGATGAGGAAGGCCTCAGGAGACCCAGCACCCAAGGCAGGGAGCCC 7776

Qy      2083 ACCGCACCCCTGTCTGAGACTGAG--GCTGCCACTTCTGGCCTCAAGAATCAGAACGATG 2140
        ||| ||||| ||||| |||| || || || | |||| |||| | ||||
Db      7777 ACCCCACCCCTGTCTGAGAATGAGGTGCCTCCTCTTTTAGCCTCAGGAATCCAAGGGATG 7836

Qy      2141 GGGACTCAGATTGCAT--GGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAG 2198
        | |||| | |||| || || || || || || || || || || ||
Db      7837 GCAACTCAGGTCAGCAGAGGGGTGGGTTCCTCAAGCCCTTCCAGGATCAAGGAAAGGAAGAC 7896

Qy      2199 GAGGGAGGACTCAGGGGACCTTGGAAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTC 2258
        ||||| ||||| |||| | ||||| ||||| |||| ||||| |||||

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[illegible]

Qy	3146	TC-CCCAAGGACCTAGGCACGTGTGGCCAGATGTTTGTCCCTCTGTCTTCCATTCTCT	3204
Db	8856	TCTTCGGAAGACCTAGGCACAGGTGGCCAGATGTGGGGTTTCTTAGGTCCT---GTTCCC	8912
Qy	3205	TATCATGGATGTGAACTCTTGATTGGATTCTCAGACCAGCAAAAGGGCAGGATCCAGG	3264
Db	8913	TCTCAGGCATGTGAGCTCTTGATCTGAGTTCTCAGGCCAGCAAAAGAGTGGGATCCAGG	8972
Qy	3265	CCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCCACTGCATGA	3324
Db	8973	CCCTGCCCTGGAGAAATGTGAGGGCCCTGAGTGAACACAGTGGGGATCATCCACTCCATGA	9032
Qy	3325	GAGTGGGGATGTCACAGAGTCCAGCCACCCTCCTGGTAGCACTGAGAAGCCAGGGCTGT	3384
Db	9033	GAGTGGGGACCTCACAGAGTCCAGCCTACCCTCTTGATGGCACTGAGGGACCGGGGCTGT	9092
Qy	3385	GCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCAGGAACCAGG	3444
Db	9093	GCTTACAGTCTGCACCCTAAGGGCCCATGGATTCTCTCTTAGGAGCTCCAGGAACAAGG	9152
Qy	3445	CAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATGCACAGGGTG	3504
Db	9153	CAGTGAGGCCTTGGTCTGAGACAGTGTCTCAGGTTACAGAGCAGAGGATGCACAGGGCTG	9212
Qy	3505	TGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCACAGGACACA	3564
Db	9213	TGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCACAAGACACA	9272
Qy	3565	TAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTTCAGTCCGTGTAATCGACCTCTG	3624
Db	9273	TAGGACTCCAAAGAGTCTGGCCTCACCTCCCTACCATCAATCCTGCAGAATCGACCTCTG	9332
Qy	3625	CTGGCCGGCTGTACCCTGA-GTACCCTCTCACTTCCTCCTTCAGGTTTTTCAGGGGACAGG	3683
Db	9333	CTGGCCGGCTATACCCTGAGGTGCTCTCACTTCCTCCTTCAGGTTCTGAGCAGACAGG	9392
Qy	3684	CCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAAGATCTGTA	3743
Db	9393	CCAACCG-GAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAAGATCTGTA	9451
Qy	3744	AGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCACACTCC	3803
Db	9452	AGTAAGCCTTTGTTAGAGCCTCTAAGATTGGTTCTCAGCTGAGGTCTCTCACATGCTCC	9511
Qy	3804	CTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCTGCCTGCTG	3863
Db	9512	CTCTCTCCGTAGGCCTGTGGGTCCCCATTGCCCAGCTTTTGCCCTGCACCTCTGCCTGCTG	9571
Qy	3864	CCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAG	3923
Db	9572	CCCTGACCAGAGTCATCATGTCTCTTGAGCAGAAGAGTCAGCACTGCAAGCCTGAGGAAG	9631
Qy	3924	CCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC-----	3975
Db	9632	GCGTTGAGGCCCAAGAAGAGGCCCTGGGCCTGGTGGGTGCACAGGCTCCTACTACTGAGG	9691
Qy	3976	-----CTCCTCCTCCTCTCCTCTGGTCCCTGGGCACCCTGGAGGAGGTGC	4019
Db	9692	AGCAGGAGGCTGCTGTCTCCTCCTCCTCTCCTCTGGTCCCTGGCACCCCTGGAGGAAGTGC	9751

Qy	4020	CCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTA	4079
Db	9752	CTGCTGCTGAGTCAGCAGGTCTCTCCCAGAGTCCTCAGGGAGCCTCTGCCTTACCCACTA	9811
Qy	4080	CCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGG	4139
Db	9812	CCATCAGCTTCACTTGCTGGAGGCAACCCAATGAGGGTTCCAGCAGCCAAGAAGAGGAGG	9871
Qy	4140	GGCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGG	4199
Db	9872	GGCCAAGCACCTCGCCTGACGCAGAGTCCTTGTTCCGAGAAGCACTCAGTAACAAGGTGG	9931
Qy	4200	CTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAG	4259
Db	9932	ATGAGTTGGCTCATTTTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCACAAAGGCAG	9991
Qy	4260	AAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTTCCTGAGATCTTCGGCAAAG	4319
Db	9992	AAATGCTGGAGAGAGTCATCAAAAATTACAAGCGCTGCTTTCCTGTGATCTTCGGCAAAG	10051
Qy	4320	CCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCC	4379
Db	10052	CCTCCGAGTCCCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCGCCAGCA	10111
Qy	4380	ACTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATC	4439
Db	10112	ACACCTACACCTTGTACCTGCCTGGGCCTTTCCTATGATGGCCTGCTGGGTAATAATC	10171
Qy	4440	AGATCATGCCCAAGACAGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCG	4499
Db	10172	AGATCTTTCCAAGACAGGCCCTTCTGATAATCGTCCTGGGCACAATTGCAATGGAGGGCG	10231
Qy	4500	GCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGA	4559
Db	10232	ACAGCGCCTCTGAGGAGGAAATCTGGGAGGAGCTGGGTGTGATGGGGGTGTATGATGGGA	10291
Qy	4560	GGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAA	4619
Db	10292	GGGAGCACACTGTCTATGGGGAGCCCAGGAACTGCTCACCCAAGATTGGGTGCAGGAAA	10351
Qy	4620	AGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGG	4678
Db	10352	ACTACCTGGAGTACCGGCAGGTACCCGGCAGTAATCCTGCGCGCTATGAGTTCCTGTGGG	10411
Qy	4679	GTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCA	4738
Db	10412	GTCCAAGGGCTCTGGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGGTCAGGGTCA	10471
Qy	4739	GTGCAAGAGTTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAG	4798
Db	10472	ATGCAAGAGTTTCGCATTGCCTACCCATCCCTGCGTGAAGCAGCTTTGTTAGAGGAGGAAG	10531
Qy	4799	AGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGG---GGACTGGGCCAGTG	4854
Db	10532	AGGGAGTCTGAGCATGAGTTGCAGCCAGGGCTGTGGGGAAGGGGCAGGGCTGGGCCAGTG	10591
Qy	4855	CACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTTCTT	4914
Db	10592	CATCTAACA--GCCCTGTGCAGCAGCTTCCCTTGCTCGTGTAAACATGAGGCCCATTTCTT	10649
Qy	4915	CACCTC---TGAAGAGAGCGGTCACTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGA	4970

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      |||||  ||||| |  ||||| ||||| ||||| || || ||||| |||
Db      10650 CACTCTGTTTGAAGAAAATAGTCAGTGTTCCTTAGTAGTGGGTTTCTATTTTGTGGATGA 10709

Qy      4971 CTTGGAGATTTATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGG 5030
      ||||| ||||| ||||| ||||| ||||| || || ||||| |||||
Db      10710 CTTGGAGATTTATCTCTGTTTCCTTTTACAATTGTTGAAATG-TTCCTTTTAATGGATGG 10768

Qy      5031 TTGAATGAAC TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATAT 5090
      ||||| ||||| ||||| ||||| ||||| || || || || ||||| |||||
Db      10769 TTGAATTAAC TTCAGCATCCAAGTTTATGAATCGTAGTTAACGTATATTGCTGTTAATAT 10828

Qy      5091 AGTTTAAGGGTAAGAGTCTTGTTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAA 5150
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      10829 AGTTTAGGAGTAAGAGTCTTGTTTTTTATTTCAGATTGGGAAATCCGTCTATTTTGTGAA 10888

Qy      5151 TTGGG---ATAATAACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAA 5207
      || || ||||| ||||| ||||| ||||| ||||| ||||| || || || ||
Db      10889 TTTGGGACATAATAACAGCAGTGGAGTAAGTATTTAGAAGTGTG---AATTCACCGTGAA 10945

Qy      5208 ATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAG 5267
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      10946 ATAGGTGAGAT-----AAATTAAGATACTTAATTCACCGCTTATGCCTCAG 10993

Qy      5268 TCTATTCTGTAAAATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGA 5327
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      10994 TCTATTCTGTAAAATTTAAAAATATATATGCATACCTGGATTTCCTTGGCTTC---GTGA 11050

Qy      5328 ATGTAAGAGAAATTAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTC 5387
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      11051 ATGTAAGAGAAATTAATCTGAATAAATAATTCTTTCTGTTAACTGGCTCATTTCTTCTC 11110

Qy      5388 CATGCACTGAGCATCTGCTTTTTGGAAGGCCCTGGGTAGTAGTGAGATGCTAAGGTAA 5447
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      11111 TATGCACTGAGCATCTGCTCTGTGGAAGGCCAGGATTAGTAGTGAGATACTAGGGTAA 11170

Qy      5448 GCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAG 5507
      ||||| || || || ||||| || || || || ||||| ||||| ||||| ||
Db      11171 GCCAGACACACACCTACCGATAGGGTATTAAGAGTCTAGGAGCGCGGTCATATAATTAAG 11230

Qy      5508 GTGGCAAGATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCT 5567
      ||| ||||| ||||| ||||| ||||| || || || ||||| ||||| |||||
Db      11231 GTGACAAGATGTCCTCTAAGATGTAGGGGAAAAGT----AACGAGTGTGGGTATGGGGCT 11286

Qy      5568 CCGGGTGAGAGTGGTGGAGTGCAATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAAAC 5627
      || ||||| ||||| || || ||||| ||||| ||||| ||||| ||||| |||||
Db      11287 CCAGGTGAGAGTGGTCGGGTGTAAATTCCTGTG-TGGGGCCTTTTGGGCTTTGGGAAAC 11345

Qy      5628 TGCAGTTCCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
      |||| || ||||| ||||| ||||| ||||| || ||||| |||
Db      11346 TGCATTTTCTTCTGAGGGATCTGATTCTAATGAAGCTTGGTGGGTCC 11392

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RESULT 6

ABQ76204

ID ABQ76204 standard; DNA; 4895 BP.

XX

AC ABQ76204;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human tumour antigen MAGE-4b DNA.

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XX
KW Tumour antigen; human; vaccine; cellular immune response; immunogen;
KW cancer; tumour; MAGE-4b; ds.
XX
OS Homo sapiens.
XX
PN US6287569-B1.
XX
PD 11-SEP-2001.
XX
PF 06-APR-1998; 98US-00056105.
XX
PR 10-APR-1997; 97US-0043467P.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Kipps TJ, Wu Y;
XX
DR WPI; 1998-583198/49.
XX
PT Generating cellular immune response in patient to target protein -
PT comprises introducing vector with nucleotide sequence encoding immunogen
PT comprising protein processing signal into cell of patient.
XX
PS Disclosure; Col 45-50; 61pp; English.
XX
CC This invention describes a novel method for generating a cellular immune
CC response in a patient to a target protein or its fragment. The method
CC involves introducing a vector containing a nucleotide sequence encoding a
CC chimeric immunogen comprising a protein processing signal and the target
CC protein or its fragment. The immunogen is produced by the cells and
CC processed so that the target protein or its fragment is presented to the
CC patients immune system and a cellular immune response is initiated. The
CC method and vectors can be used as a form of vaccination and could be used
CC to generate a cellular immune response in patients to, e.g. cancerous
CC tumours. The cellular immune response is the predominant immune response
CC in the patient. This sequence represents a DNA fragment which encodes the
CC human tumour antigen MAGE-4b described in the method of the invention.
CC Note: The information in this spec has been previously disclosed in
CC WO199845444 however this spec contained no sequence information
XX
SQ Sequence 4895 BP; 1134 A; 1235 C; 1433 G; 1093 T; 0 U; 0 Other;

Query Match          44.3%; Score 2513.6; DB 2; Length 4895;
Best Local Similarity 79.9%; Pred. No. 0;
Matches 3415; Conservative 0; Mismatches 694; Indels 165; Gaps 32;

Qy 1478 ATGGTTCTGAGGGGCGGCTTGAGATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAG 1537
    || || ||||| ||||| ||||| || || ||||| |||
Db 607 ATAGTCCTGAGGGGCCAGTTGAGATCGGCTGAGGGGAGCGGGCCCAAGCTCTGTGGCGAG 666

Qy 1538 GCAAGGTGAGATGCTGAGGGAGGACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAA 1597
    ||||| ||||| ||||| ||||| ||||| || |||| || || ||
Db 667 GCAAGGTGAGACTCTGAGGAAGGACTGAGGAGGCCCCACCCAAGATAGA-GGAACCCAA 725

Qy 1598 ATGATCCAGTACCACCCCTGCTGCCAGCCCTGGACCACCCGCCAGGACAGATGTCTCAG 1657
    || ||||| || ||||| ||||| ||||| || || |||||
Db 726 ATAATCCAGCCCACGTCTGCTGCCAGTCTGGACCACCCGG---GGGAAGACTTCTCA- 781

Qy 1658 CTGGACCACCCCGTCCCGTCCCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATA 1717
    || || || || ||||| ||||| || || ||||| |||||

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Db	782	---GGCTAGGCCATCCCAGTCCCCACTGCCACTAAAGCTACAGGGGACTCTAGAGTCA--	836
Qy	1718	GCTTATGTGACCGGGGCAGGGTTGGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGC	1777
Db	837	-----AGAGCTTGGTGTGCCCAAGGCAGGGCCAGG	866
Qy	1778	ATCCGCCCCGGCATTAGGGTCAGGACCCTGGGAGGGAACTGAGGGTCCCCACCCACACCT	1837
Db	867	CTCTGCCTGGCATCGGGTCAGGACCTTGAGAGGGAACTGAGGGCGCTACACCCCCACCC	926
Qy	1838	GTCTCCTCATCTCCACCGCCACCCCACTCACATTCCCATACCTACCCCCTACCCCCAACC	1897
Db	927	CATCCGCATTC-----CAACATGCCCAGCCCCATCCCCAACTCCGTTTTCAGAA	976
Qy	1898	TCATCTTGTGAGAATCCCTGCTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCAC	1957
Db	977	TCCATTTT---TCCCCTGCAGTCAACCCCGGAAGACCTGGGAATGGT---CAGGCAC	1029
Qy	1958	TCGGATCTTGACGTCCCCATCCAGGGTCTGATGGAGGGAAGGG-----GCTTGAACAG	2010
Db	1030	TCGGATCTTGACATCCACATCGAGGGCTGAAGGAGGGAGAGAGTTTGGTATCATGAGCAG	1089
Qy	2011	GGCCTCAGGGGAGCAGAGGGAG-----GGCCCTACTGCGAGATGAGGGAGGCCTCAGAG	2064
Db	1090	AGCCTCAGGGTAGCAGAGGGAGGACCCTGGCCCTCTGGGAGATGAGGAAGGCCTCAGGA	1149
Qy	2065	GACCCAGCACCC-----TAGGACACCGCACCCCTGTCTGAGACTGAG--GCTGCCA	2113
Db	1150	GACCCAGCACCCCAAGGCAGGGAGCCACCCACCCCTGTCTGAGAATGAGGTGCCTCTCT	1209
Qy	2114	CTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGGGTGGGA--CCCAG	2171
Db	1210	CCTTTAGCCTCAGGAATCCAAGGGATGGCAACTCAGGTCAGCAGAGGGGTGGGTTCAG	1269
Qy	2172	GCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTTGGAAATCCAGAT	2231
Db	1270	CCCTTCCAGGATCAAGGAAAGGAAGACGAGGGAGGATTTCAGGGGGCCTTGCATTCCAGAT	1329
Qy	2232	CAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATGGCCCATATTTTC	2291
Db	1330	CAGTGGAGACCTGGGCCCTGGGAGGTCTGGGCAAGGTAGCCACCTGTAGCTCATACTTC	1389
Qy	2292	CTGCATCTTTGAGGT----GACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTC	2347
Db	1390	CTGCATCTTCGAGGTCACAGAGAGGAGAGGGCTATGGTCTGAGGGGTGGTACTTCAGGTC	1449
Qy	2348	AACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCC-CCCTTCATGAGGACT	2406
Db	1450	CGCAGAGGGAGGAGTCCCAGGATCTACAGGACCCAAGGTGTGCCACACTTCACGAGGAAT	1509
Qy	2407	GGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCTTTTAGTA	2466
Db	1510	GGGGATACCTGTGGCTCAGAAAGACGGGACCCACAGAGTCTGGCTGTCCCTGTCTCTTA	1569
Qy	2467	GCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCACAGGCA	2526
Db	1570	GCTCAGGGGGGACCAGAGGAGGGATGGCCCTATGTGCCAATTTCACTTGTTCACAGGCA	1629
Qy	2527	GGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCTACTCAT	2586
Db	1630	GGAAGTTGGGGGAACCTTCAGGGAGATGAGGTTTTGGAGTAAAGGGGGCAATGTTTGCTCAT	1689

Qy	2587	GTCAGGGAATTGGGGGTTGAGGAAGCACAGGCCTGGCAGGAATAAAGATGAGTGAGACA	2646
Db	1690	CTCAGGGGGTTGGGGGTTGAGGAAGGGCAGGCCCTGTCAGGAGCAAACATGAGT-ACCCA	1748
Qy	2647	GACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTCAGCCCTGGACACCTCACCC	2706
Db	1749	CAGGAGGCCATCAGAACCCCTCACCCCAGAACCAGGGGTCAGCCCTGGGCACCCACAC	1808
Qy	2707	AG-----GATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGAC	2758
Db	1809	AGGGGTGACAGGATGTGGCTCCTTCTCATTCTGATTCCAGATCTCAGTGAGGTGAGGAC	1868
Qy	2759	CTCATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAG	2818
Db	1869	CTTGTTCTCAGAGGGTGACTCAGGTCAACACAGGGACCCCATCTGGTCTACAGACACAG	1928
Qy	2819	CGGTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCC	2878
Db	1929	TGGTCCCAGGATCTGCCAAGAGTCCTGGTGAGGAATGTGAGGGAGGATTGAGGGTACCAC	1988
Qy	2879	AGGACCAGAACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCCCAG	2938
Db	1989	AGGGCCAGAACGCAGATGATGACCCACAGAAATCAGCCCTGCTCCTGTTGTACCCCCAG	2048
Qy	2939	AGAGCATGGGCTGGGCCGCTGCGGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAG	2998
Db	2049	AGAGCATGGGCTTGGCTTCTGCTGAGGTCCCTCTCTTATCCTGGGATCACTGGTGTAC	2108
Qy	2999	GGACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGG	3058
Db	2109	GGAGGGGGAGGCCTTGGTCTGAGGGGGCTGCACCCAGGTCAGTAGAGGGAGGGTCCCAGG	2168
Qy	3059	CCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCA	3118
Db	2169	CTCTGCCAGGAGTTGAGGTGAGGACCAAGCAGGCTCCGCATCCAGGACACATGGGTTC	2228
Qy	3119	ATGAATTTTGATATCTCTTGCTGCCCTTC-CCCAAGGACCTAGGCACGTGTGGCCAGATG	3177
Db	2229	ATGAATTTGACATCTTTTGCTGTCTGCTTCTTCGGAAGACCTAGGCACAGGTGGCCAGATG	2288
Qy	3178	TTTGTCCCTCCTGTCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCT	3237
Db	2289	TGGGGTTTCTTAGGTCCT---GTTCCCTCTCAGGCATGTGAGCTCTTGATCTGAGTTTCT	2345
Qy	3238	CAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAATATAAGGGCCCTGCGTGA	3297
Db	2346	CAGGCCAGCAAAAGAGTGGGATCCAGGCCCTGCCTGGAGAAATGTGAGGGCCCTGAGTGA	2405
Qy	3298	GAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTC	3357
Db	2406	ACACAGTGGGGATCATCCACTCCATGAGAGTGGGGACCTCACAGAGTCCAGCCTACCTC	2465
Qy	3358	CTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCAGGCTGACCCCTGAGGGCCCGTGGATT	3417
Db	2466	TTGATGGCACTGAGGGACCGGGCTGTGCTTACAGTCTGCACCCTAAGGGCCCATGGATT	2525
Qy	3418	CCTCTTCTGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAG	3477
Db	2526	CCTCTCTAGGAGCTCCAGGAACAAGGCAGTGAGGCCTTGGTCTGAGACAGTGTCTCAG	2585

Qy 3478 GTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGGCCTGAATGCACAC 3537  
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 Db 2586 GTTACAGAGCAGAGGATGCACAGGCTGTGCCAGCAGTGAATGTTTGGCCTGAATGCACAC 2645

Qy 3538 CAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTC TGGCCTCACCTCCCTA 3597  
 |||||  
 Db 2646 CAAGGGCCCCACCTGCCACAAGACACATAGGACTCCAAAGAGTC TGGCCTCACCTCCCTA 2705

Qy 3598 CTGTCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGA-GTACCCTCTCACT 3656  
 | ||| |||||  
 Db 2706 CCATCAATCCTGCAGAATCGACCTCTGCTGGCCGGCTATACCCTGAGGTGCTCTCTCACT 2765

Qy 3657 TCCTCCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCAC 3716  
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 Db 2766 TCCTCCTTCAGGTTCTGAGCAGACAGGCCAA-CCGGAGGACAGGATTCCCTGGAGGCCAC 2824

Qy 3717 AGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACT 3776  
 |||||  
 Db 2825 AGAGGAGCACCAAGGAGAAGATCTGTAAGTAAGCCTTTGTTAGAGCCTCTAAGATTGGT 2884

Qy 3777 TCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCC 3836  
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 Db 2885 TCTCAGCTGAGGTCTCTCACATGCTCCCTCTCTCCGTAGGCCTGTGGGTCCCCATTGCCC 2944

Qy 3837 AGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGA 3896  
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 Db 2945 AGCTTTTGCCTGCACCTTGCCTGCTGCCCTGAGCAGAGTCATCATGTCTCTTGAGCAGA 3004

Qy 3897 GGAGTCTGCAC TGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG 3956  
 |||||  
 Db 3005 AGAGTCAGCACTTGCAAGCCTGAGGAAGGCGTTGAGGCCCAAGAAGAGGCCCTGGGCCTGG 3064

Qy 3957 TGTGTGTGCAGGCTGCCAC-----CTCCTCCTCCTCTCCTC 3992  
 || ||| |||||  
 Db 3065 TGGGTGCGCAGGCTCCTACTACTGAGGAGCAGGAGGCTGCTGTCTCCTCCTCCTCTCCTC 3124

Qy 3993 TGGTCCTGGGCACCTTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTC 4052  
 |||||  
 Db 3125 TGGTCCCTGGCACCTTGGAGGAAGTGCTGCTGCTGAGTCAGCAGGTCTCCCCAGAGTC 3184

Qy 4053 CTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTG 4112  
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 Db 3185 CTCAGGGAGCCTCTGCCTTACCCACTACCATCAGCTTCACTTGCTGGAGGCAACCCAATG 3244

Qy 4113 AGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGT 4172  
 |||||  
 Db 3245 AGGGTTCCAGCAGCCAAGAAGAGGAGGGGCCAAGCACCTCGCCTGACGCAGAGTCCTTGT 3304

Qy 4173 TCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATC 4232  
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 Db 3305 TCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGCTCATTTTCTGCTCCGCAAGTATC 3364

Qy 4233 GAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGC 4292  
 |||||  
 Db 3365 GAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGAGAGTCATCAAAAATTACAAGC 3424

Qy 4293 ACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGACAGCTGGTCTTTGGCATTG 4352  
 |||  
 Db 3425 GCTGCTTTCTGATCTTCGGCAAAGCCTCCGAGTCCCTGAAGATGATCTTTGGCATTG 3484

Qy 4353 ACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCT 4412



Db	3485	ACGTGAAGGAAGTGGACCCACCAGCAACACCTACACCCTTGTCACCTGCCTGGGCCTTT	3544
Qy	4413	CCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCCTTCCTGATAATTG	4472
Db	3545	CCTATGATGGCCTGCTGGGTAATAATCAGATCTTTCCCAAGACAGGCCTTCCTGATAATCG	3604
Qy	4473	TCCTGGTCATGATTGCAATGGAGGGCGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGC	4532
Db	3605	TCCTGGGCACAATTGCAATGGAGGGCGACAGCGCCTCTGAGGAGGAAATCTGGGAGGAGC	3664
Qy	4533	TGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGC	4592
Db	3665	TGGGTGTGATGGGGGTGTATGATGGGAGGGAGCACACTGTCTATGGGGAGCCCAGGAAAC	3724
Qy	4593	TGCTCACCCAAGATTTGGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTG	4651
Db	3725	TGCTCACCCAAGATTTGGGTGCAGGAAAAC TACCTGGAGTACCGGCAGGTACCCGGCAGTA	3784
Qy	4652	ATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGA	4711
Db	3785	ATCCTGCGCGCTATGAGTTCCTGTGGGGTCCAAGGGCTCTGGCTGAAACCAGCTATGTGA	3844
Qy	4712	AAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGC	4771
Db	3845	AAGTCCTGGAGCATGTGGTCAGGGTCAATGCAAGAGTTCGCATTGCCTACCCATCCCTGC	3904
Qy	4772	GTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCA	4831
Db	3905	GTGAAGCAGCTTTGTTAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAGGGCTG	3964
Qy	4832	GTGGGAGGG----GGACTGGGCCAGTGCACCTTCAGGGCCGCGTCCAGCAGCTTCCCTT	4887
Db	3965	TGGGGAAGGGGCAGGGCTGGGCCAGTGCATCTAACA--GCCCTGTGCAGCAGCTTCCCTT	4022
Qy	4888	GCCTCGTGTGACATGAGGCCCATTTCTTCACTC----TGAAGAGAGCGGTCACTGTTCTCA	4943
Db	4023	GCCTCGTGTAAACATGAGGCCCATTTCTTCACTCTGTTTGAAGAAAATAGTCAGTGTCTTA	4082
Qy	4944	GTAGTAGGTTTCTGTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGGAATT	5003
Db	4083	GTAGTGGGTTTCTATTTTGTGGATGACTTGGAGATTTATCTCTGTTTCCTTTTACAATT	4142
Qy	5004	GTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGTTTATGAATG	5063
Db	4143	GTTGAAATG-TTCCTTTTAATGGATGGTTGAATTAACCTCAGCATCCAAGTTTATGAATC	4201
Qy	5064	ACAGCAGTCACACAGTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAG	5123
Db	4202	GTAGTTAACGTATATTGCTGTTAATATAGTTTAGGAGTAAGAGTCTTGTTTTTATTTCAG	4261
Qy	5124	ATTGGGAAATCCATTCTATTTTGTGAATTGGG---ATAATAACAGCAGTGGAATAAGTAC	5180
Db	4262	ATTGGGAAATCCGTTCTATTTTGTGAATTTGGGACATAATAACAGCAGTGAGTAAGTAT	4321
Qy	5181	TTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATTAAGAG	5240
Db	4322	TTAGAAGTGTG---AATTCACCGTGAATAGGTGAGAT-----AAATTAAGAG	4366
Qy	5241	ATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTTAAAGATATATGCAT	5300

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Db      4367 ATACTTAATCCCCGCTTATGCCTCAGTCTATTCTGTAAAATTTAAAAATATATATGCAT 4426

Qy      5301 ACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAGAATTC 5360
        |||||
Db      4427 ACCTGGATTTCCTTGGCTTC---GTGAATGTAAGAGAAATTAAATCTGAATAAATAATTC 4483

Qy      5361 TTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAAGGCCCT 5420
        || |||||
Db      4484 TTTCGTGTTAACTGGCTCATTTCTTCTCTATGCACTGAGCATCTGCTCTGTGGAAGGCCCA 4543

Qy      5421 GGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCGTAGAG 5480
        || |||||
Db      4544 GGATTAGTAGTGGAGATACTAGGGTAAGCCAGACACACACCTACCGATAGGGTATTAAGA 4603

Qy      5481 TCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGGGAAAA 5540
        | ||| ||| |||||
Db      4604 GTCTAGGAGCGCGTTCATATAATTAAGGTGACAAGATGTCCTCTAAGATGTAGGGGAAAA 4663

Qy      5541 GTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCATGCCCTGA 5600
        || | ||| |||||
Db      4664 GT----AACGAGTGTGGGTATGGGGCTCCAGGTGAGAGTGGTCGGGTGTAAATTCCCTGT 4719

Qy      5601 GCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCCTTCTGGGGGAGCTGATTGTAATGA 5660
        | |||||
Db      4720 G-TGGGGCCTTTTGGGCTTTGGGAAACTCCATTTTCTTCTGAGGGATCTGATTCTAATGA 4778

Qy      5661 TCTTGGGTGGATCC 5674
        | |||||
Db      4779 AGCTTGGTGGGTCC 4792

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# RESULT 7

ADS73099

ID ADS73099 standard; cDNA; 4895 BP.

XX

AC ADS73099;

XX

DT 18-NOV-2004 (first entry)

XX

DE Human kidney tumour specific cDNA, SEQ ID 1696.

XX

KW Human; ss; kidney tumour; kidney cancer; cytostatic; gene therapy;

KW T-cell; immune response.

XX

OS Homo sapiens.

XX

PN US2003109434-A1.

XX

PD 12-JUN-2003.

XX

PF 19-MAR-2002; 2002US-00102524.

XX

PR 19-MAR-2001; 2001US-0277245P.

PR 21-DEC-2001; 2001US-0343340P.

XX

PA (CORI-) CORIXA CORP.

XX

PI Algate PA, Mannion J, Gaiger A, Gordon B, Harlocker SL;

XX

DR WPI; 2002-759855/82.

XX

PT New isolated polynucleotides and polypeptides, useful for detecting the  
PT presence of, and treating cancer, particularly kidney cancer by  
PT stimulating T-cells specific for a tumor protein, and stimulating immune  
PT response in a patient.

XX

PS Claim 1; SEQ ID NO 1696; 78pp; English.

XX

CC The invention relates to a new isolated polynucleotide (a Human kidney  
CC tumour specific cDNA) comprising any one of the 1855 sequences identified  
CC in the specification (or their complements, degenerate variants,  
CC sequences consisting of at least 20 contiguous residues them, sequences  
CC that hybridise to them under highly stringent conditions or sequences  
CC having at least 75 or 90% sequence identity to the 1855 sequences. Also  
CC included are detecting/determining the presence of cancer in a patient,  
CC stimulating an immune response in a patient; treating kidney cancer in a  
CC patient, an isolated polypeptide encoded by one of the 1855 sequences, an  
CC expression vector comprising the polynucleotide operably linked to an  
CC expression control sequence, a host cell transformed/transfected with the  
CC vector, an isolated antibody (or its antigen-binding fragment) that  
CC specifically binds to the protein, a fusion protein comprising at least  
CC one the proteins, stimulating and/or expanding T-cells specific for a  
CC tumour protein, an isolated T-cell population comprising the T-cells, a  
CC composition comprising a first component (such as a carrier or  
CC immunostimulant) and a second component (comprising one of the  
CC polynucleotides, the polypeptides, an antibody, T-cell or an antigen-  
CC presenting cell that expresses the polynucleotide) and a diagnostic kit  
CC comprising at least one of the oligonucleotides, or at least one antibody  
CC and a detection reagent comprising a reporter group. The polynucleotides,  
CC polypeptides, antibodies and antigen-presenting cells are useful for  
CC detecting the presence of, and treating cancer, particularly kidney  
CC cancer by stimulating and/or expanding T-cells specific for a tumour  
CC protein, and stimulating immune response in a patient. The present  
CC sequence is one of the Human kidney tumour specific cDNAs. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from USPTO  
CC at seqdata.uspto.gov/sequence.html?DocID=20030109434.

XX

SQ Sequence 4895 BP; 1134 A; 1235 C; 1433 G; 1093 T; 0 U; 0 Other;

Query Match 44.3%; Score 2513.6; DB 7; Length 4895;  
Best Local Similarity 79.9%; Pred. No. 0;  
Matches 3415; Conservative 0; Mismatches 694; Indels 165; Gaps 32;

Qy 1478 ATGTTCTGAGGGGCGGCTTGAGATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAG 1537  
|| || ||||| ||||| ||||| || ||||| || ||||| ||  
Db 607 ATAGTCCTGAGGGGCCAGTTGAGATCGGCTGAGGGGAGCGGGCCCAAGCTCTGTGGCGAG 666  
  
Qy 1538 GCAAGGTGAGATGCTGAGGGAGGACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAA 1597  
||||||| ||||| ||||| ||||| || ||||| || ||||| ||  
Db 667 GCAAGGTGAGACTCTGAGGAAGGACTGAGGAGGCCCCACCCAAGATAGA-GGAACCCAA 725  
  
Qy 1598 ATGATCCAGTACCACCCCTGCTGCCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAG 1657  
|| ||||| | ||||| ||||| ||||| || ||||| |||||  
Db 726 ATAATCCAGCCCACGTCTGCTGCCAGTCTGGACCACCCGG---GGGAAGACTTCTCA- 781  
  
Qy 1658 CTGGACCACCCCGTCCCGTCCCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATA 1717  
| | | | | ||||| ||||| || ||||| || ||||| |||||  
Db 782 ---GGCTAGGCCATCCCAGCTCCCACTGCCACTAAAGCTACAGGGGACTCTAGAGTCA-- 836  
  
Qy 1718 GCTTATGTGACCGGGGCAGGGTTGGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGC 1777  
|||| || | |||||

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Db      837 -----AGAGCTTGGTGTGCCCCAAGGCAGGGCCAGG 866
Qy      1778 ATCCGCCCCGGCATTAGGGTCAGGACCTTGGGAGGGAAC TGAGGGTTCCCCACCCACACCT 1837
      || ||| ||||| ||||| ||| ||||| ||||| | ||||| ||||
Db      867 CTCTGCCTGGCATCGGGTCAGGACCTTGAGAGGGAAC TGAGGGCGCTACACCCCCACCC 926
Qy      1838 GTCTCCTCATCTCCACCGCCACCCCACTCACATTCCCATACCTACCCCTACCCCCAACC 1897
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      927 CATCCGCATTC-----CAACATGCCCAGCCCCATCCCCAACTCCGTTTTGCAGAA 976
Qy      1898 TCATCTTGTCAGAATCCCTGCTGTCAACCCACGGAAGCCACGGAATGGCGGCCAGGCAC 1957
      || || |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      977 TCCATTTTT----TCCCCTGCAGTCAACCCGGAAGACCTGGGAATGGT---CAGGCAC 1029
Qy      1958 TCGGATCTTGACGTCCCCATCCAGGGTCTGATGGAGGGAAGGG-----GCTTGAACAG 2010
      ||||| ||||| ||| |||| |||| |  |  |  |  |  |  |  |
Db      1030 TCGGATCTTGACATCCACATCGAGGGCTGAAGGAGGGAGAGAGTTTGGTATCATGAGCAG 1089
Qy      2011 GGCCTCAGGGGAGCAGAGGGAG-----GGCCCTACTGCGAGATGAGGGAGGCCTCAGAG 2064
      ||||| ||||| ||||| ||||| ||| ||||| ||||| ||||| ||
Db      1090 AGCCTCAGGGTAGCAGAGGGAGGACCTGGCCCTCTGGGAGATGAGGAAGGCCTCAGGA 1149
Qy      2065 GACCCAGCACCC-----TAGGACACCGCACCCCTGTCTGAGACTGAG--GCTGCCA 2113
      ||||| ||||| ||  |||| ||||| ||||| |||| |  |  |
Db      1150 GACCCAGCACCCAAGGCAGGGAGCCACCCACCCCTGTCTGAGAATGAGGTGCCTCCT 1209
Qy      2114 CTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGGGTGGGA--CCCAG 2171
      |  |  | ||||| |||| |  |||| ||||| |  |  | ||| || |||
Db      1210 CCTTTAGCCTCAGGAATCCAAGGGATGGCAACTCAGGTCAGCAGAGGGGTGGGTTCGAAG 1269
Qy      2172 GCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTTGAATCCAGAT 2231
      ||| | ||| |  |  |  ||||| ||||| ||||| |||| |  |||||
Db      1270 CCCTTCCAGGATCAAGGAAAGGAAGACGAGGGAGGATTCAGGGGGCCTTGCAATCCAGAT 1329
Qy      2232 CAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATGGCCCATATTTTC 2291
      |||| |  |||| ||||| ||||| |||| ||| |||| |  |  | |||| |||
Db      1330 CAGTGGAGACCTGGGCCCTGGGAGGTCTGGGCAAGGTAGCCACCTGTAGCTCATACTTC 1389
Qy      2292 CTGCATCTTTGAGGT----GACAGGACAGAGCTGTGGTCTGAGAAAGTGGGGCCTCAGGTC 2347
      ||||| |||| |  || |||| || || ||||| |||| |  |||||
Db      1390 CTGCATCTTCGAGGTACAGAGAGGAGAGGGCTATGGTCTGAGGGGTGGTACTTCAGGTC 1449
Qy      2348 AACAGAGGGAGGAGTTCAGGATCCATATGGCCCAAGATGTGCC-CCCTTCATGAGGACT 2406
      ||||| ||||| ||||| |  |  | ||||| |||| |  |||| |  ||||
Db      1450 CGCAGAGGGAGGAGTCCCAGGATCTACAGGACCAAGGTGTGCCACACTTCACGAGGAAT 1509
Qy      2407 GGGGATATCCCCGGCTCAGAAAAGAGGACTCCACACAGTCTGGCTGTCCCTTTTAGTA 2466
      ||||| |  ||||| ||||| |||| |||| ||||| ||||| || |||
Db      1510 GGGGATACCTGTGGCTCAGAAAGACGGGACCCACAGAGTCTGGCTGTCCCTGTCTCTTA 1569
Qy      2467 GCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCACAGGCA 2526
      |||| ||||| ||||| ||||| |||| ||| |  ||||| ||||| ||||
Db      1570 GCTCAGGGGGGACCAGAGGAGGGATGGCCCTATGTGCCAATTCCTTGTTCACAGGCA 1629
Qy      2527 GGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGATGTCTACTCAT 2586
      ||||| |||| |  ||||| |||| ||| |||| |||| |  |||||
Db      1630 GGAAGTTGGGGAACCTTCAGGGAGATGAGGTTTGGAGTAAAGGGGCAATGTTTGCTCAT 1689
Qy      2587 GTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGTGAGACA 2646
      ||||| ||||| ||||| |||| ||| |||| ||| ||||| |  |||
Db      1690 CTCAGGGGGTTGGGGTTGAGGAAGGGCAGGCCCTGTCAGGAGCAACATGAGT-ACCCA 1748

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[illegible]

Qy	3538	CAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTA	3597
Db	2646	CAAGGGCCCCACCTGCCACAAGACACATAGGACTCCAAAGAGTCTGGCCTCACCTCCCTA	2705
Qy	3598	CTGTCACTCCTGTAGAAATCGACCTCTGCTGGCCGGCTGTACCCTGA-GTACCCTCTCACT	3656
Db	2706	CCATCAATCCTGCAGAATCGACCTCTGCTGGCCGGCTATACCCTGAGGTGCTCTCTCACT	2765
Qy	3657	TCCTCCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCAC	3716
Db	2766	TCCTCCTTCAGGTTCTGAGCAGACAGGCCAA-CCGGAGGACAGGATTCCCTGGAGGCCAC	2824
Qy	3717	AGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACT	3776
Db	2825	AGAGGAGCACCAAGGAGAAGATCTGTAAGTAAGCCTTTGTTAGAGCCTCTAAGATTTGGT	2884
Qy	3777	TCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCC	3836
Db	2885	TCTCAGCTGAGGTCTCTCACATGCTCCCTCTCTCCGTAGGCCTGTGGGTCCCCATTGCCC	2944
Qy	3837	AGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGA	3896
Db	2945	AGCTTTTGCCCTGCACTCTTGCCCTGCTGCCCTGAGCAGAGTCATCATGTCTCTTGAGCAGA	3004
Qy	3897	GGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG	3956
Db	3005	AGAGTCAGCACTGCAAGCCTGAGGAAGGCGTTGAGGCCCAAGAAGAGGCCCTGGGCCTGG	3064
Qy	3957	TGTGTGTGCAGGCTGCCAC-----CTCCTCCTCCTCTCCTC	3992
Db	3065	TGGGTGCGCAGGCTCCTACTACTGAGGAGCAGGAGGCTGCTGTCTCCTCCTCCTCTCCTC	3124
Qy	3993	TGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTC	4052
Db	3125	TGGTCCCTGGCACCTTGAGGAAGTGCCCTGCTGCTGAGTCAGCAGGTCTCCCCAGAGTC	3184
Qy	4053	CTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTG	4112
Db	3185	CTCAGGGAGCCTCTGCCTTACCCACTACCATCAGCTTCACTTGCTGGAGGCAACCCAATG	3244
Qy	4113	AGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGT	4172
Db	3245	AGGGTTCCAGCAGCCAAGAAGAGGAGGGGCCAAGCACCTCGCCTGACGCAGAGTCCTTGT	3304
Qy	4173	TCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATC	4232
Db	3305	TCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGCTCATTTTCTGCTCCGCAAGTATC	3364
Qy	4233	GAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGC	4292
Db	3365	GAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGAGAGTCATCAAAAATTACAAGC	3424
Qy	4293	ACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGACAGCTGGTCTTTGGCATTG	4352
Db	3425	GCTGCTTTCTGTGATCTTCGGCAAAGCCTCCGAGTCCCTGAAGATGATCTTTGGCATTG	3484
Qy	4353	ACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCT	4412
Db	3485	ACGTGAAGGAAGTGGACCCACCGACCAACACCTACACCCTTGTACCTGCCTGGGCCTTT	3544
Qy	4413	CCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTG	4472

Db	3545	 CCTATGATGGCCTGCTGGGTAATAATCAGATCTTTCCCAAGACAGGCCTTCTGATAATCG	3604
Qy	4473	TCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGC	4532
Db	3605	 TCCTGGGCACAATTGCAATGGAGGGCGACAGCGCCTCTGAGGAGGAAATCTGGGAGGAGC	3664
Qy	4533	TGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGC	4592
Db	3665	 TGGGTGTGATGGGGGTGTATGATGGGAGGGAGCACACTGTCTATGGGGAGCCCAGGAAAC	3724
Qy	4593	TGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTG	4651
Db	3725	 TGCTCACCCAAGATTTGGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTACCCGGCAGTA	3784
Qy	4652	ATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGA	4711
Db	3785	 ATCCTGCGCGCTATGAGTTCTGTGGGGTCCAAGGGCTCTGGCTGAAACCAGCTATGTGA	3844
Qy	4712	AAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTCTTCCCATCCCTGC	4771
Db	3845	 AAGTCCTGGAGCATGTGGTCAGGGTCAATGCAAGAGTTCGCATTGCCTACCCATCCCTGC	3904
Qy	4772	GTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCA	4831
Db	3905	 GTGAAGCAGCTTTGTTAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAGGGCTG	3964
Qy	4832	GTGGGAGGG----GGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCTT	4887
Db	3965	 TGGGGAAGGGGCAGGGCTGGGCCAGTGCATCTAACA--GCCCTGTGCAGCAGCTTCCCTT	4022
Qy	4888	GCCTCGTGTGACATGAGGCCCATTCCTTCACTC----TGAAGAGAGCGGTGAGTGTCTCA	4943
Db	4023	 GCCTCGTGTAAACATGAGGCCCATTCCTTCACTCTGTTTGAAGAAAATAGTCAGTGTCTTA	4082
Qy	4944	GTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGGAATT	5003
Db	4083	 GTAGTGGGTTTCTATTTTGTTGGATGACTTGGAGATTTATCTCTGTTTCTTTTACAATT	4142
Qy	5004	GTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGTTTATGAATG	5063
Db	4143	 GTTGAAATG-TTCCTTTTAATGGATGGTTGAATTAAC TTCAGCATCCAAGTTTATGAATC	4201
Qy	5064	ACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAG	5123
Db	4202	 GTAGTTAACGTATATTGCTGTTAATATAGTTTAGGAGTAAGAGTCTGTTTTTTATTTCAG	4261
Qy	5124	ATTGGGAAATCCATTCTATTTTGTGAATTGGG---ATAATAACAGCAGTGGAATAAGTAC	5180
Db	4262	 ATTGGGAAATCCGTTCTATTTTGTGAATTGGGACATAATAACAGCAGTGAGTAAGTAT	4321
Qy	5181	TTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAATTAAGAG	5240
Db	4322	 TTAGAAGTGTG---AATTCACCGTGAAATAGGTGAGAT-----AAATTAAGAG	4366
Qy	5241	ATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATATGCAT	5300
Db	4367	 ATACTTAATTCCCGCCTTATGCCTCAGTCTATTCTGTAAAATTTAAAAATATATATGCAT	4426
Qy	5301	ACCTGGATTTCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAGAAATTC	5360

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Db      4427 ACCTGGATTTCTTGGCTTC---GTGAATGTAAGAGAAATTAAATCTGAATAAATAATTC 4483
Qy      5361 TTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAAGGCCCT 5420
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4484 TTTCTGTTAACTGGCTCATTCTTCTCTATGCACTGAGCATCTGCTCTGTGGAAGGCCCA 4543
Qy      5421 GGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCGTAGAG 5480
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4544 GGATTAGTAGTGGAGATACTAGGGTAAGCCAGACACACCTACCGATAGGGTATTAAGA 4603
Qy      5481 TCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGGGAAAA 5540
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4604 GTCTAGGAGCGCGGTCATATAATTAAGGTGACAAGATGTCTCTAAGATGTAGGGAAAA 4663
Qy      5541 GTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGCCCTGA 5600
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4664 GT----AACGAGTGTGGGTATGGGGCTCCAGGTGAGAGTGGTCGGGTGTAAATTCCTGT 4719
Qy      5601 GCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTGTAATGA 5660
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4720 G-TGGGGCCTTTTGGGCTTTGGGAAACTCCATTTTCTTCTGAGGGATCTGATTCTAATGA 4778
Qy      5661 TCTTGGGTGGATCC 5674
      | ||||| |||
Db      4779 AGCTTGGTGGGTCC 4792

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# RESULT 8

ADW41953

ID ADW41953 standard; cDNA; 4895 BP.

XX

AC ADW41953;

XX

DT 24-MAR-2005 (first entry)

XX

DE cDNA elevated in kidney tumor cells SEQ ID NO 1696.

XX

KW gene therapy; diagnosis; pharmaceutical; cancer; cytostatic;

KW genitourinary disease; neoplasm; renal tumor; gene; ss..

XX

OS Unidentified.

XX

PN WO200274237-A2.

XX

PD 26-SEP-2002.

XX

PF 19-MAR-2002; 2002WO-US010055.

XX

PR 19-MAR-2001; 2001US-0277245P.

PR 21-DEC-2001; 2001US-0343340P.

XX

PA (CORI-) CORIXA CORP.

XX

PI Algate PA, Mannion J, Gaiger A, Gordon B, Harlocker SL;

XX

DR WPI; 2002-759855/82.

XX

PT New isolated polynucleotides and polypeptides, useful for detecting the

PT presence of, and treating cancer, particularly kidney cancer by

PT stimulating T-cells specific for a tumor protein, and stimulating immune

PT response in a patient.



XX  
PS Claim 13; SEQ ID NO 1696; 252pp; English.

The invention describes a new isolated polynucleotide (I) comprising: any one of the 1855 sequences identified in the specification; complements or degenerate variants of (a); sequences consisting of at least 20 contiguous residues of (a); sequences that hybridize to (a) under highly stringent conditions; or sequences having at least 75 or 90% sequence identity to (a). Also described are: detecting (M1) or determining the presence of cancer in a patient; stimulating (M2) an immune response in a patient; treating (M3) kidney cancer in a patient; an isolated polypeptide (II) encoded by (I) and comprising, or having at least 70 or 90% sequence identity to, any one of the 8 sequences identified in the specification; an expression vector (III) comprising (I) operably linked to an expression control sequence; a host cell (IV) transformed or transfected with (III); an isolated antibody (V) or its antigen-binding fragment that specifically binds to (II); a fusion protein (VI) comprising at least one (II); an oligonucleotide (VII) that hybridizes to the nucleotide sequences cited above under highly stringent conditions; stimulating (M4) and/or expanding T-cells specific for a tumor protein; an isolated T-cell population (VIII) comprising the T-cells in (M4); a composition (IX) comprising a first component such as a carrier or immunostimulant and a second component comprising (I), the polypeptide encoded by (I), an antibody or its antigen-binding fragment that specifically binds to (II), (VI), or an antigen-presenting cell that expresses the polynucleotide; and a diagnostic kit (X) comprising at least one of the oligonucleotide, or at least one antibody and a detection reagent comprising a reporter group. The polynucleotides, polypeptides, antibodies and antigen-presenting cells are useful for detecting the presence of, and treating cancer, particularly kidney cancer by stimulating and/or expanding T-cells specific for a tumor protein, and stimulating immune response in a patient. This sequence represents a kidney tumour cDNA, expression of which is increased in kidney tumors.

SQ Sequence 4895 BP; 1134 A; 1235 C; 1433 G; 1093 T; 0 U; 0 Other;

Query Match 44.3%; Score 2513.6; DB 7; Length 4895;  
Best Local Similarity 79.9%; Pred. No. 0;  
Matches 3415; Conservative 0; Mismatches 694; Indels 165; Gaps 32;

Qy	1478	ATGGTTC TGAGGGGCGGCTTGAGATCCACTGAGGGGAGTGGTTT TAGGCTCTGTGAGGAG	1537
Db	607	ATAGTCCTGAGGGGCCAGTTGAGATCGGCTGAGGGGAGCGGGCCCAAGCTCTGTGGCGAG	666
Qy	1538	GCAAGGTGAGATGCTGAGGGAGGACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAA	1597
Db	667	GCAAGGTGAGACTCTGAGGAAGGACTGAGGAGGCCCCCACCCAAGATAGA-GGAACCCAA	725
Qy	1598	ATGATCCAGTACCACCCCTGCTGCCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAG	1657
Db	726	ATAATCCAGCCACGTCCTGCTGCCAGTCTCTGGACCACCCGG---GGGAAGACTTCTCA-	781
Qy	1658	CTGGACCACCCCCCGTCCCGTCCCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATA	1717
Db	782	---GGCTAGGCCATCCCAGCTCCCACTGCCACTAAAGCTACAGGGGACTCTAGAGTCA--	836
Qy	1718	GCTTATGTGACCGGGGCAGGGTTGGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGC	1777
Db	837	-----AGAGCTTGGTGTGCCCAAGGCAGGGCCAGG	866

Qy 1778 ATCCGCCCGGCATTAGGGTCAGGACCCTGGGAGGGAAGTGAAGGTTCCCCACCCACACCT 1837  
 || ||| |||| | |||| |||| | |||| |||| | |||| ||||  
 Db 867 CTCTGCCTGGCATCGGGTCAGGACCTTGAGAGGGAAGTGAAGGCGCTACACCCCCACCC 926

Qy 1838 GTCTCCTCATCTCCACCGCCACCCCACTCACATTCCCATACCTACCCCTACCCCAACC 1897  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 927 CATCCGCATTC-----CAACATGCCAGCCCCATCCCCAACTCCGTTTTGCAGAA 976

Qy 1898 TCATCTTGTCAGAATCCCTGCTGTCAACCCACGGAAGCCACGGAATGGCGGCCAGGCAC 1957  
 || | | | | | | | | | | | | | | | | | | | | | |  
 Db 977 TCCATTTTT----TCCCCTGAGTCAACCCCGGAAGACCTGGGAATGGT---CAGGCAC 1029

Qy 1958 TCGGATCTTGACGTCCCCATCCAGGGTCTGATGGAGGGAAGGG-----GCTTGAACAG 2010  
 ||||| |||| | |||| | |||| | | | | | | | | | | | | | | | | |  
 Db 1030 TCGGATCTTGACATCCACATCGAGGGCTGAAGGAGGGAGAGAGTTTGGTATCATGAGCAG 1089

Qy 2011 GGCCTCAGGGGAGCAGAGGGAG-----GGCCCTACTGCGAGATGAGGGAGGCCTCAGAG 2064  
 ||||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||  
 Db 1090 AGCCTCAGGGTAGCAGAGGGAGGACCCTGGCCCTCCTGGGAGATGAGGAAGGCCTCAGGA 1149

Qy 2065 GACCCAGCACCC-----TAGGACACCGCACCCCTGTCTGAGACTGAG--GCTGCCA 2113  
 ||||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||  
 Db 1150 GACCCAGCACCCCAAGGCAGGGAGCCACCCACCCCTGTCTGAGAATGAGGTGCCTCCT 1209

Qy 2114 CTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGGGTGGGA--CCCAG 2171  
 | | | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||  
 Db 1210 CCTTTAGCCTCAGGAATCCAAGGGATGGCAACTCAGGTCAGCAGAGGGGTGGGTTCAG 1269

Qy 2172 GCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTTGGGAATCCAGAT 2231  
 ||| | || | | | | |||| | |||| | |||| | |||| | |||| | |||| | ||||  
 Db 1270 CCCTTCCAGGATCAAGGAAAGGAAGACGAGGGAGGATTCAGGGGGCCTTGCATTCCAGAT 1329

Qy 2232 CAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATGGCCCATATTTTC 2291  
 |||| | || | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||  
 Db 1330 CAGTGGAGACCTGGGCCCTGGGAGGTCTGGGCAAGGTAGCCACCTGTAGCTCATACTTC 1389

Qy 2292 CTGCATCTTTGAGGT----GACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTC 2347  
 ||||| |||| | || | || | || | || | || | || | || | || | || | || | || | ||  
 Db 1390 CTGCATCTTCGAGGTCACAGAGAGGAGAGGGCTATGGTCTGAGGGGTGGTACTTCAGGTC 1449

Qy 2348 AACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCC--CCCTTCATGAGGACT 2406  
 ||||| |||| | || | || | || | || | || | || | || | || | || | || | || | ||  
 Db 1450 CGCAGAGGGAGGAGTCCCAGGATCTACAGGACCAAGGTGTGCCACACTTCACGAGGAAT 1509

Qy 2407 GGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTTTTAGTA 2466  
 ||||| | | ||||| |||| | || | || | || | || | || | || | || | || | || | ||  
 Db 1510 GGGGATACCTGTGGCTCAGAAAGACGGGACCCACAGAGTCTGGCTGTCCCCTGTTCTTA 1569

Qy 2467 GCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCACAGGCA 2526  
 |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||  
 Db 1570 GCTCAGGGGGGACCAGAGGAGGGATGGCCCTATGTGCCAATTTCACTTGTTCACAGGCA 1629

Qy 2527 GGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCTACTCAT 2586  
 ||||| || | ||||| |||| | || | || | || | || | || | || | || | || | || | ||  
 Db 1630 GGAAGTTGGGAACCTTCAGGGAGATGAGGTTTTGGAGTAAAGGGGCAATGTTTGCTCAT 1689

Qy 2587 GTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGTGAGACA 2646  
 |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||  
 Db 1690 CTCAGGGGGTTGGGGGTTGAGGAAGGGCAGGCCCTGTCAGGAGCAAACATGAGT-ACCCA 1748

Qy 2647 GACAAGGCTATTGGAATCCACACCCCAAGAAAGGGGTGAGCCCTGGACACCTCACCC 2706

Db	1749	CAGGAGGCCATCAGAACCCCTACCCCCAGAACCAAGGGGTCAGCCCTGGGCACCCACAC	1808
Qy	2707	AG-----GATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGAC	2758
Db	1809	AGGGGTGACAGGATGTGGCTCCTTCTCATTTCTGATTCCAGATCTCAGTGAGGTGAGGAC	1868
Qy	2759	CTCATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAG	2818
Db	1869	CTTGTTCTCAGAGGGTGACTCAGGTCAACACAGGGACCCCATCTGGTCTACAGACACAG	1928
Qy	2819	CGGTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCC	2878
Db	1929	TGGTCCCAGGATCTGCCAAGAGTCCTGGTGAGGAATGTGAGGGAGGATTGAGGGTACCAC	1988
Qy	2879	AGGACCAGAACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTACCCACAG	2938
Db	1989	AGGGCCAGAACGCAGATGATGACCCACAGAAATCAGCCCTGCTCCTGTTGTACCCACAG	2048
Qy	2939	AGAGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAG	2998
Db	2049	AGAGCATGGGCTTGGCTTCTGCTGAGGTCCCTCTCTTATCCTGGGATCACTGGTGTAC	2108
Qy	2999	GGACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGG	3058
Db	2109	GGAGGGGGAGGCCCTTGGTCTGAGGGGGCTGCACCCAGGTCAGTAGAGGGAGGGTCCCAGG	2168
Qy	3059	CCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCA	3118
Db	2169	CTCTGCCAGGAGTTGAGGTGAGGACCAAGCAGGCTCCGCATCCAGGACACATGGGTTCCA	2228
Qy	3119	ATGAATTTTGATATCTCTTGCTGCCCTTC-CCCAAGGACCTAGGCACGTGTGGCCAGATG	3177
Db	2229	ATGAATTTTCGACATCTTTTGCTGTCTTCTTCCGAAGACCTAGGCACAGGTGGCCAGATG	2288
Qy	3178	TTTGTCCCTCCTGTCTTCCATTCTTATCATGGATGTGAACCTTGATTGGATTCT	3237
Db	2289	TGGGGTTTCTTAGGTCCT--GTTCCCTCTCAGGCATGTGAGCTCTTGATCTGAGTTTCT	2345
Qy	3238	CAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGA	3297
Db	2346	CAGGCCAGCAAAAGAGTGGGATCCAGGCCCTGCCTGGAGAAATGTGAGGGCCCTGAGTGA	2405
Qy	3298	GAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTC	3357
Db	2406	ACACAGTGGGGATCATCCACTCCATGAGAGTGGGGACCTCACAGAGTCCAGCCTACCTC	2465
Qy	3358	CTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCTGAGGGCCCGTGGATT	3417
Db	2466	TTGATGGCACTGAGGGACCGGGCTGTGCTTACAGTCTGCACCTAAGGGCCCATGGATT	2525
Qy	3418	CCTCTTCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAG	3477
Db	2526	CCTCTCTAGGAGCTCCAGGAACAAGGCAGTGAGGCCTTGGTCTGAGACAGTGTCTCAG	2585
Qy	3478	GTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACAC	3537
Db	2586	GTTACAGAGCAGAGGATGCACAGGCTGTGCCAGCAGTGAATGTTGCCCTGAATGCACAC	2645
Qy	3538	CAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTA	3597

Db	2646	CAAGGGCCCCACCTGCCCACAAGACACATAGGACTCCAAAGAGTCTGGCCTCACCTCCCTA	2705
Qy	3598	CTGTCTAGTCCTGTAGAAATCGACCTCTGCTGGCCGGCTGTACCCTGA-GTACCTCTCACT	3656
Db	2706	CCATCAATCTTGCAGAATCGACCTCTGCTGGCCGGCTATACCCTGAGGTGCTCTCTCACT	2765
Qy	3657	TCCTCTTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCAC	3716
Db	2766	TCCTCTTTCAGGTTCTGAGCAGACAGGCCAA-CCGGAGGACAGGATTCCCTGGAGGCCAC	2824
Qy	3717	AGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACT	3776
Db	2825	AGAGGAGCACCAAGGAGAAGATCTGTAAGTAAGCCTTTGTTAGAGCTCTAAGATTGGT	2884
Qy	3777	TCTCAGCTGAGGCCTCTCACACATCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCC	3836
Db	2885	TCTCAGCTGAGGTCTCTCACATGCTCCCTCTCTCCGTAGGCCTGTGGGTCCCCATTGCC	2944
Qy	3837	AGCTCCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGA	3896
Db	2945	AGCTTTTGCCTGCACTCTTGCCTGCTGCCCTGAGCAGAGTCATCATGTCTTCTGAGCAGA	3004
Qy	3897	GGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG	3956
Db	3005	AGAGTCAGCACTGCAAGCCTGAGGAAGCGTTGAGGCCCAAGAAGAGGCCCTGGGCCTGG	3064
Qy	3957	TGTGTGTGCAGGCTGCCAC-----CTCCTCCTCCTCTCCTC	3992
Db	3065	TGGGTGCGCAGGCTCCTACTACTGAGGAGCAGGAGGCTGCTGTCTCCTCCTCCTCTCCTC	3124
Qy	3993	TGGTCTTGGGCACCTTGGAGGAGGTGCCACTGCTGGGTCAACAGATCTCCCCAGAGTC	4052
Db	3125	TGGTCCCTGGGCACCTTGGAGGAAGTGCTGCTGCTGAGTCAGCAGGTCTCCCCAGAGTC	3184
Qy	4053	CTCAGGGAGCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTG	4112
Db	3185	CTCAGGGAGCTCTGCCTTACCCACTACCATCAGCTTCACTTGCTGGAGGCAACCCAATG	3244
Qy	4113	AGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCTTGAGTCCTTGT	4172
Db	3245	AGGGTTCCAGCAGCCAAGAAGAGGAGGGGCCAAGCACCTCGCCTGACGCAGAGTCCTTGT	3304
Qy	4173	TCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATC	4232
Db	3305	TCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGCTCATTTTCTGCTCCGCAAGTATC	3364
Qy	4233	GAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGC	4292
Db	3365	GAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGAGAGTGTATCAAAAATTACAAGC	3424
Qy	4293	ACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGACAGCTGGTCTTTGGCATTG	4352
Db	3425	GCTGCTTTCTGTGATCTTCGGCAAAGCCTCCGAGTCCCTGAAGATGATCTTTGGCATTG	3484
Qy	4353	ACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCT	4412
Db	3485	ACGTGAAGGAAGTGGACCCACAGCAACCTTACACCTTGTCACCTGCCTGGGCCTTT	3544
Qy	4413	CCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTG	4472
Db	3545	CCTATGATGGCCTGCTGGGTGATAATCAGATCTTTCCCAAGACAGGCTTCCTGATAATCG	3600

Qy	4473	TCCTGGTTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGC	4532
Db	3605		
Qy	4533	TCCTGGGCACAATTGCAATGGAGGGCGACAGCGCCTCTGAGGAGGAAATCTGGGAGGAGC	3664
Qy	4533	TGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGC	4592
Db	3665		
Qy	4593	TGGGTGTGATGGGGGTGTATGATGGGAGGGAGCACACTGTCTATGGGGAGCCCAGGAAAC	3724
Qy	4593	TGCTCACCCAAGATTGGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTG	4651
Db	3725		
Qy	4652	TGCTCACCCAAGATTGGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTACCCGGCAGTA	3784
Qy	4652	ATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGA	4711
Db	3785		
Qy	4712	ATCCTGCGCGCTATGAGTTCCTGTGGGGTCCAAGGGCTCTGGCTGAAACCAGCTATGTGA	3844
Qy	4712	AAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGC	4771
Db	3845		
Qy	4772	AAGTCCTGGAGCATGTGGTCAGGGTCAATGCAAGAGTTCGCATTGCCTACCCATCCCTGC	3904
Qy	4772	GTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCA	4831
Db	3905		
Qy	4832	GTGAAGCAGCTTTGTTAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAGGGCTG	3964
Qy	4832	GTGGGAGGG----GGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCTT	4887
Db	3965		
Qy	4888	TGGGGAAGGGGCAGGGCTGGGCCAGTGCATCTAACA--GCCCTGTGCAGCAGCTTCCCTT	4022
Qy	4888	GCCTCGTGTGACATGAGGCCCATTTCTTCACTC----TGAAGAGAGCGGTCAGTGTCTCA	4943
Db	4023		
Qy	4944	GCCTCGTGTAAACATGAGGCCCATTTCTTCACTCTGTTTGAAGAAAATAGTCAGTGTCTTA	4082
Qy	4944	GTAGTAGGTTTCTGTTCATTTGGGTGACTTGGAGATTTATCTTTGTTCCTTTTGGGAATT	5003
Db	4083		
Qy	5004	GTAGTGGGTTTCTATTTTGTGGATGACTTGGAGATTTATCTCTGTTTCCTTTTACAATT	4142
Qy	5004	GTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAGTTTCAAGTTCAGCATCCAAGTTTATGAATG	5063
Db	4143		
Qy	5064	GTTGAAATG-TTCCTTTTAATGGATGGTTGAATTAAGTTTCAAGTTCAGCATCCAAGTTTATGAATC	4201
Qy	5064	ACAGCAGTCACACAGTTCTGTGTATATAGTTTAAAGGGTAAGAGTCTGTGTTTTATTTCAG	5123
Db	4202		
Qy	5124	GTAGTTAACGTATATTGCTGTTAATATAGTTTAGGAGTAAGAGTCTGTGTTTTATTTCAG	4261
Qy	5124	ATTGGGAAATCCATTCTATTTTGTGAATTGGG---ATAATAACAGCAGTGGAATAAGTAC	5180
Db	4262		
Qy	5181	ATTGGGAAATCCGTTCTATTTTGTGAATTTGGGACATAATAACAGCAGTGAGTAAGTAT	4321
Qy	5181	TTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATTAAGAG	5240
Db	4322		
Qy	5241	TTAGAAGTGTG---AATTCACCGTGAAATAGGTGAGAT-----AAATTAAG	4366
Qy	5241	ATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATATGCAT	5300
Db	4367		
Qy	5301	ATACTTAATTCGCCCTTATGCCTCAGTCTATTCTGTAAAATTTAAAAATATATATGCAT	4426
Qy	5301	ACCTGGATTTCCTTGCCCTTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAAGAAATTC	5360
Db	4427		
Qy	5360	ACCTGGATTTCCTTGCCCTTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAATAATTC	4483

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Qy      5361 TTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGGAAGGCCCT 5420
        || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4484 TTTCTGTTAACTGGCTCATTCTTCTCTATGCACTGAGCATCTGCTCTGTGGAAGGCCCA 4543

Qy      5421 GGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCGTAGAG 5480
        || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4544 GGATTAGTAGTGGAGATACTAGGGTAAGCCAGACACACCTACCGATAGGGTATTAAGA 4603

Qy      5481 TCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGGGAAAA 5540
        |  || |||| |||| |||| ||||| ||||| ||||| ||||| |||||
Db      4604 GTCTAGGAGCGCGGTCAATAATTAAGGTGACAAGATGTCTCTAAGATGTAGGGGAAAA 4663

Qy      5541 GTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGCCCTGA 5600
        ||  || || |||| |||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4664 GT----AACGAGTGTGGGTATGGGGCTCCAGGTGAGAGTGGTCGGGTGTAAATTCCTGT 4719

Qy      5601 GCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTGTAATGA 5660
        | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4720 G-TGGGGCCTTTTGGGCTTTGGGAAACTCCATTTTCTTCTGAGGGATCTGATTCTAATGA 4778

Qy      5661 TCTTGGGTGGATCC 5674
        | ||||| |||
Db      4779 AGCTTGGTGGGTCC 4792

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RESULT 9

ABQ76206

ID ABQ76206 standard; DNA; 4736 BP.

XX

AC ABQ76206;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human tumour antigen MAGE-5b DNA.

XX

KW Tumour antigen; human; vaccine; cellular immune response; immunogen;

KW cancer; tumour; MAGE-5b; ds.

XX

OS Homo sapiens.

XX

PN US6287569-B1.

XX

PD 11-SEP-2001.

XX

PF 06-APR-1998; 98US-00056105.

XX

PR 10-APR-1997; 97US-0043467P.

XX

PA (REGC ) UNIV CALIFORNIA.

XX

PI Kipps TJ, Wu Y;

XX

DR WPI; 1998-583198/49.

XX

PT Generating cellular immune response in patient to target protein -

PT comprises introducing vector with nucleotide sequence encoding immunogen

PT comprising protein processing signal into cell of patient.

XX

PS Disclosure; Col 54-58; 61pp; English.

XX

CC This invention describes a novel method for generating a cellular immune

CC response in a patient to a target protein or its fragment. The method  
 CC involves introducing a vector containing a nucleotide sequence encoding a  
 CC chimeric immunogen comprising a protein processing signal and the target  
 CC protein or its fragment. The immunogen is produced by the cells and  
 CC processed so that the target protein or its fragment is presented to the  
 CC patients immune system and a cellular immune response is initiated. The  
 CC method and vectors can be used as a form of vaccination and could be used  
 CC to generate a cellular immune response in patients to, e.g. cancerous  
 CC tumours. The cellular immune response is the predominant immune response  
 CC in the patient. This sequence represents a DNA fragment which encodes the  
 CC human tumour antigen MAGE-5b described in the method of the invention.  
 CC Note: The information in this spec has been previously disclosed in  
 CC WO199845444 however this spec contained no sequence information

XX

SQ Sequence 4736 BP; 1114 A; 1278 C; 1304 G; 1040 T; 0 U; 0 Other;

Query Match 42.8%; Score 2429.6; DB 2; Length 4736;  
 Best Local Similarity 75.9%; Pred. No. 0;  
 Matches 3736; Conservative 0; Mismatches 869; Indels 315; Gaps 47;

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Qy      715 TTCCCGCCAGGAACATCCGGGTGCCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGG 774
          ||| ||||| || | ||||| || ||||| ||||| ||||| ||||| |||
Db      15 TTCAACCCAGGGAATCCCTGGGTGACCAGATGTGGTGCCACTGTCTTGACATTGTGAGGT 74

Qy      775 CAGAGAGAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGA 834
          | ||||| ||| | ||| |||| | || | ||| || | ||| |||
Db      75 CGGAGAGAAGCAAGGGCCTCGCTCTCAGGGGCAGC-TGGAGATCAGCTGAGGGCAGCTGG 133

Qy      835 CCCAGGCTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTC 894
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Db      134 CCCTGGCTCTGTGAGGATGCAAGGTGAGATGCTGAGGGAGGACTAAGGAGTATCCACCC 193

Qy      895 CAAATAGAGAGCCCCAAATATTCCAG---CCCCGCCCTTGCTGCCAGCCCTGGCCACCC 951
          | ||| | ||||| ||||| ||| | ||| ||||| ||| ||| |||
Db      194 CTGGTAGTGACCCCAAATAATCCAGTGCCACCTCTCCTGCTGCTAGCTCTGGACCATCC 253

Qy      952 GCGGGAAGACGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGAC 1011
          || | ||| ||| || ||||| ||||| |||| | | ||||| |||
Db      254 AGGGCAGGACTTCTTAGGCTGGGCCACCCCCAGTCCCCCACCCTTAAGCCGCAGGGGA- 312

Qy      1012 ACCAGGTTCTTCTCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGT 1071
          ||| ||| ||||| ||| | ||||| ||||| ||||| |||
Db      313 -----CTCAGGAGACAGAGCTTGGTATGACCAGGGCAGGACTGGT 352

Qy      1072 TAGGAGAGGGCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGC 1131
          ||||| ||| || | ||||| ||||| ||| ||| ||| ||| |||
Db      353 TAGGAGAGGACAGCTCCA-GCTCTGCCAGGAAACAACGTCAGGAACCTAAGGGAAAGCT 411

Qy      1132 TGTGGGCCCCCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCC 1191
          | ||||
Db      412 GAGGCTACCC----- 422

Qy      1192 CACCCAACCCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCAC 1251
          |||| | | | | ||| |||| | |
Db      423 -----CACCCAAACTCTATTCTGTCCCTACCTCCGTCC 457

Qy      1252 CTGACCACCACCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCCTCACT 1311
          | ||| ||||| ||| || ||| |||| | | ||||| |||
Db      458 CCCACCTACACCCCATTC-----CCACCCCTTCCCTACCGGCACCTCTATCCCACA 512

Qy      1312 GCCCCCAACCCACCCCTCATCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATCTCTG 1371

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Db	513	TCCCCCA-----	CCCCTATCCTG	530
Qy	1372	GCAGAATCCGGTT-TGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAA	1430	
Db	531	GCAGAATCCGATTCTGCCCCCTGATTTCAACCCAGGGAAGCCCTAGGGGGCCGGATGTGAT	590	
Qy	1431	ACCACTGACTTGAACCTCACAGATCTGAGAGAAGCCAGGTTTCATTTAATGGTTCTGAGGG	1490	
Db	591	GCTGCTGACTTGTGCAATTGGGGGTCAGAGAGAATCAAGG-----GCATGGTTCTGAGAA	644	
Qy	1491	GCGGCTTGAGATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATG	1550	
Db	645	GCCGACTGAGATCAGCAGAGGGGAATGGGCCCGGGCTCTGTGAGGAGGCAAGGTGAGACC	704	
Qy	1551	CT-GAGGGAGGACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTAC	1609	
Db	705	CCCGAGGAAGGAATGAGGAAGCCCTCACCC--AGATAGAGAACCCCAAATAATCCAGTAC	762	
Qy	1610	CACCCCTGCTGCCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCC	1669	
Db	763	TACCTCTGCTGCCAGCCCTGGACCAC----CCAGGGCAGACTTCTCAGGCTGAACCTTCC	818	
Qy	1670	CCGTCCCGTCCCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTT-ATGTGAC	1728	
Db	819	C---CCCTCCCCACTGCCACTTAAGCCACAAGGGACTCTGGAGTCAGACCTTGGTGTGAC	875	
Qy	1729	CGGGGCAGGGTTGGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGC	1788	
Db	876	CAGGGAAGGGCCGGTCAGGAGAGG-----GCAGGGCCAGGCTCTGTGTCAGGC	922	
Qy	1789	ATTAGGGTCAGGACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATC	1848	
Db	923	ATCAAAATCAGGACCCTGAGAGAGAATTGAGGGCCCCCACCACAACCCCTATACCCATCC	982	
Qy	1849	TCCACCGCCACCCCACTCACATTCCCATACCTACC----CCCTACCCCCAACCTCATCTT	1904	
Db	983	CTAACCCCATACCCACTCTACTTGCATTCCAGCCCCATCCCCACACCTTACCCCATCTT	1042	
Qy	1905	GTCAGAA-----TCCCTGCTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGG	1954	
Db	1043	GGCAGAATCTGTTTCTTTCCCTGCAGTCAACCCACAGAAGCCCCAGGAATGACAGACAGG	1102	
Qy	1955	CAC TCGGATCTTGACGTCCCCATCCAGGGTCTGATGGAGGGAAGGG-----GCTTGAA	2007	
Db	1103	CACACCCATTCTGACGTCCACATCCAGGGCTGAAGGAGGGAAGGGCTTAGTATCATGAG	1162	
Qy	2008	CAGGGCCTCAGGGGAGCAGAGG----GAGGGCCCTACTGCGAGATGAGGGAGGCCCTCAGA	2063	
Db	1163	CAGGGCCTCAGGGGAGTCTCTGCTCCTCAAGCCCTGCTGGGAGTAAAGGGAGGCCCTCAGG	1222	
Qy	2064	GGACCCAGCACCCTAGGA-----CACCGCACCCCTGTCTGAGACTGAGGC--TGCC	2112	
Db	1223	GAACCCAGGTCCTCAGGATAGGGGGTCCACTCCAACCTGTCTGAGACTGAGGCGCCTCC	1282	
Qy	2113	ACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGGGTGGGACCCAGG	2172	
Db	1283	TCTTTCATCTCGGGAATCACAGGGATGGAGACTCACGTCAGCAGAGGGTGGGGCCCAAC	1342	
Qy	2173	CCTGCAAGGCTTACGCGGAGGAAGAGGAGGAGGACTCAGGGGACCTTGGAAATCCAGATC	2232	



Db 1343 CCTGCCAGGATCAAGGAGAGGAAGAAGAGGGAGGACTCAGGGTACCTTTGAGTCCAGAAC 1402

Qy 2233 AGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATGGCCCATATTTCC 2292  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1403 AATGGGGACCTTTGCCCTGGGAGGTCCAGTGCACAGTGGCCACCTGTAGCCCATGCTTGC 1462

Qy 2293 TGCATCTTTGAGGTGAC----AGGACAGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTCA 2348  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1463 TGCACCTTCTGGGTGACAAAGAGGAGAGGGCTGTGGTCAGAGCAGTGGTGACTCAGGTCA 1522

Qy 2349 ACAGAGGGAGGAGTTCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATGAGGACTGG 2408  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1523 GCAGAGGGAGGAGTCCAGCATCTGCAGGCCCAATGTGTGCCCCATTCATGAAGATTGG 1582

Qy 2409 GGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTTTTAGTAGC 2468  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1583 GGACA-CCTTGGCTCAGAAAGAAGGGACCCACAGAGTCTGGCTGTCCCCTGATTTTTGC 1641

Qy 2469 TCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCCTTGTACCACAGGCAGG 2528  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1642 TCAGAGGGGACCAAATCAAGGATAGCCCTATGTGCCAACCTCATTTGTGCCACAGGAAAG 1701

Qy 2529 AAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCTACTCATGT 2588  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1702 AAGTTGAAGAGCCCTCAGGGTGATGGGGTCTTGCAGTAAAGGGGAGCTATCTGCTCATCT 1761

Qy 2589 CAGGGAATTGGGGGTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGTGAGACAGA 2648  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1762 CAGGGGGTTTCAGGTTGAGGAATGGCAGGCCCATCACGATGAAGAGTAACCCACAGG-- 1819

Qy 2649 CAAGGCTATTGGAATCCACACCCCAAGAAAGGGGTCAGCCCTGGACACCTCA----- 2703  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1820 ---AGCCATAGAAACACTCACCCCAAGAAAGGGGTCATACCTGGACACCCCATGTGG 1876

Qy 2704 ----CCCAGGATGTGGCTTCTTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACC 2759  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1877 GGGTGACAGGATGTAGCT-CCATCTCATTCCTGTTTTCAGATCTCGGGGAGGTGAGGAAC 1935

Qy 2760 TCATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGC 2819  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1936 TTGTTCTCCGAGGATGACTCAGGTCAACACAGGGGCCCCCATCTGGTGGATAGACAGAGT 1995

Qy 2820 GGTCCCAGGATCTGCCATGCGTTCCGGTGAGGAACATGAGGGAGGACTGAGGGTACCCCA 2879  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1996 GGTCCCAGGATCTGTCTAGTAGTTCCGGTGAGGAACATGAGGGACGATTGAGGGCACCTT 2055

Qy 2880 GGACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCCA 2939  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 2056 GGGCCAGAACACAGATGAGGACCTCACGGAATCTGCCCTGCCCTGCTGTCACTCCAGA 2115

Qy 2940 GAGCATGGGCTGGGCCGTCTGCCGAGGTCTTCC--GTTATCCTGGGATCATTGATGTCA 2997  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 2116 GAGCATGGGCAGGGCTGTCTGCTGCAGTCCCCCCTTACCCTGGGATCATTGGTGTCA 2175

Qy 2998 GGGACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAG 3057  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 2176 GTGATGGGGAGGTCTTTGTC-GAGGGGTCTGCACTCAGGTCAGTAGAGGGAGCGTCTTAG 2234

Qy 3058 GCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGACCTCACCCAGGACACATTAATTCC 3117  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 2235 GCCCTGCCAGGAGACAAGGTAAGAACGAAGCAGGTTCTCACCCAGGACACATGAATTCC 2294

Qy	3118	AATGAATTTTGATATCTCTTGCTGCCCTTCCCCA-AGGACCTAGGCACGTGTGGCCAGAT	3176
Db	2295	AATGCATTTTCAGCATCTCTTCTGTCTTCCCAAGAGGACCTGGGCACGTGTGGCCAGAT	2354
Qy	3177	GTTTGTCCCCTCCTGTCTTCCATTCCCTTATCATGGATGTGAACTCTTGATTGATTTC	3236
Db	2355	GTGAGTCTCCTCATGTCTCT--GTTCCCTATCAGGGATGTGAGCTCTTAATCTGAGTTTC	2411
Qy	3237	TCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTG	3296
Db	2412	TCAGGCCAGCAAAAGGGTGGGATCCAGGCCCTGCCAGGAGAAAGGTGAGGGCCCTGTGTG	2471
Qy	3297	AGAACAGAGGGGGTCACTCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCT	3356
Db	2472	AGCACAGAGGGGACCATTCACCCCAAGAGGGTGGAGACCTCACAGATTCCAGCCTACCT	2531
Qy	3357	CCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGAT	3416
Db	2532	CCTGTTAGCACTGGGGGCTGAGGCTGTGCTTGCCAGTCTGCACCCTGAGGGCCCATGCAT	2591
Qy	3417	TCCTCTTCTGAGCTCCAGGAACCAGGCAGTGAGGCCCTGGTCTGAGACAGTATCTCTCA	3476
Db	2592	TCCTCTTCCAGGAGCTCCAGGAAACAGACACTGAGGCCCTGGTCTGAGGCCGTGCCCTCA	2651
Qy	3477	GGTCACAGAGCAGAGGATGCACAGGGT---GTGCCAGCAGTGAATGTTGCCCTGAATG	3532
Db	2652	GGTCACAGAGCAGAGGAGATGCAGACGTCTAGTGCCAGCAGTGAACGTTGCCCTGAATG	2711
Qy	3533	CACACCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCA-CC	3591
Db	2712	CACACTAATGGCCCCCATCGCCCCAGAACATATGGGACTCCAGAGCACCTGGCCTCACCC	2771
Qy	3592	TCCCTACTGTGAGTCTGTAGAACGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTC	3651
Db	2772	TCTCTACTGTGAGTCTGTGAGAATCAGCCTCTGCTTGCTTGCTGTACCCTGAGGTGCCCTC	2831
Qy	3652	TCACTTCCTCCTTCAGGTTTTCAGGGGACAGGCCAACCCAGAGGAC-----A	3698
Db	2832	TCACTTTTTCCTTCAGGTTCTCAGGGGACAGGCTGACCAGGATCACCAGGAAGCTCCAGA	2891
Qy	3699	GGATTCCCTGGAGGCCACAGAGGAGCACC-AAGGAGAAGATCTGTAAGTAGGCCTTTGTT	3757
Db	2892	GGATCCCCAGGAGGCCCTAGAGGAGCACCAAGGAGAAGATCTGTAAGTAAGCCTTTGTT	2951
Qy	3758	AGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGC	3817
Db	2952	AGAGCCTCCAAGGTTTCAGTTTTCAGCTGAGGCTTCTCACATGCTCCCTCTCTCTCCAGGC	3011
Qy	3818	CTGTGGGTCTTCATTGCCAGCTCCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTC	3877
Db	3012	CAGTGGGTCTCCATTGCCAGCTCCTGCCACACTCCTGCCTGTTGCGGTGACCAGAGTC	3071
Qy	3878	ATCATGTCTCTTGAGCAGAGGAGTCTGCAAGCCTGAGGAAGCCCTTGAGGCCCAA	3937
Db	3072	GTCATGTCTCTTGAGCAGAAGAGTCAGCACTGCAAGCCTGAGGAAGCCCTTGACACCAA	3131
Qy	3938	CAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC-----C	3976
Db	3132	GAAGAGGCCCTGGGCCTGGTGGGTGTGCAGGCTGCCACTACTGAGGAGCAGGAGGCTGTG	3191

Qy 3977 TCCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACA 4036  
 |||  
 Db 3192 TCCTCCTCCTCTCCTCTGGTCCCAGGCACCCTGGGGGAGGTGCCTGCTGCTGGGTACCA 3251

Qy 4037 GATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCCTTCCCACTACCATCAACTTCACTCGA 4096  
 | ||||| | |||  
 Db 3252 GGTCTCTCAAGAGTCCTCAGGGAGCCTCCGCCATCCCCACTGCCATCGATTTCACCTCTA 3311

Qy 4097 CAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGT 4156  
 ||||| ||| | ||| ||||| |||  
 Db 3312 TGGAGGCAATCCATTAAGGGCTCCAGCAACCAAGAAGAGGAGGGGCCAAGCACCTCCCCT 3371

Qy 4157 ATCCTGGAGTCCTTGTTCAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTTT 4216  
 || ||||| ||||| ||| ||| ||||| ||| ||| |||||  
 Db 3372 GACCCAGAGTCTGTGTTCAGCAGCACTCAGTAAGAAGGTGGCTGACTTGATTCATTTT 3431

Qy 4217 CTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTC 4276  
 ||||| ||| || || ||||| ||||| ||||| ||||| |||  
 Db 3432 CTGCTCCTCAAGTATTAAGTCAAGGAGCCGGTCACAAAGGCAGAAATGCTGGAGAGCGTC 3491

Qy 4277 ATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAG 4336  
 ||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 3492 ATCAAAAATTACAAGCGCTGCTTCTCTGAGATCTTCGGCAAAGCCTCCGAGTCCTTGCAG 3551

Qy 4337 CTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCTTGTGTC 4396  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 3552 CTGGTCTTTGGCATTGACGTGAAGGAAGCGGACCCACCGAACACCTACACCCTTGTGTC 3611

Qy 4397 ACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACA 4456  
 ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 3612 ACCTGCCTGGG--ACTCCTATGATGGCCTGGTGGTT--TAATCAGATCATGCCCAAGACG 3667

Qy 4457 GGCTTCTTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAG 4516  
 ||| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 3668 GGCCTCCTGATAATCGTCTTGGGCATGATTGCAATGGAGGGCAAATGCGTCCCTGAGGAG 3727

Qy 4517 GAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTAT 4576  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 3728 AAAATCTGGGAGGAGCTGGGTGTGATGAAGGTGTATGTTGGGAGGGAGCACAGTGTCTGT 3787

Qy 4577 GGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGGC 4636  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 3788 GGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGC 3847

Qy 4637 AGGTGCCGACAGTGATCCCGCAGCTATGAGTTCCGTGTTGGGTCCAAGGGCCCTCGCTG 4696  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 3848 AGGTGCCCAGCAGTGATCCCATATGCTATGAGTTACTGTGGGTCCAAGGGCACTCGCTG 3907

Qy 4697 AAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAAGAGTTTCGCTTTT 4756  
 ||||| || ||| || ||| ||||| ||||| ||||| ||||| |||||  
 Db 3908 CT-----TGAAAGTACTGGAGCACGTGGTCAGGGTCAATGCAAGAGTTCTCATTT 3957

Qy 4757 TCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAG 4816  
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 3958 CCTACCCATCCCTGCATGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAG 4017

Qy 4817 TTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCTCCAG 4876  
 ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||  
 Db 4018 CTGCAGCCAGGGCCACTGCGAGGGGGCTGGGCCAGTGCACCTTCCAGGGCTCCGTCAG 4077

Qy 4877 CAGCTTCCCCTGCC--TCGTGTGACATGAGGCCATTCTTCACTC--TGAAGAGAGCGGTC 4933

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      || ||||| || | ||||| ||||| ||| ||||| |||
Db      4078 TAGTTTCCCTGCCTTAATGTGACATGAGGCCATTCTCTCTCTTTGAAGAGAGCAGTC 4137
Qy      4934 AGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTC 4993
      | ||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Db      4138 AACATTCTTAGTAGTGGGTTTCTGTTCTATTGGATGACTTTGAGATTTGTCTTTGTTTCC 4197
Qy      4994 TTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAG 5053
      ||||| ||||| || ||||| || ||||| ||||| ||||| |||
Db      4198 TTTTGGGAATTGTTCAAATG-TTCCTTTTAATGGGTGGTTGAATGAACTTCAGCATTCAAA 4256
Qy      5054 TTTATGAATGACAGCAGTCACAC--AGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTG 5111
      ||||| ||||| ||||| ||| ||| ||||| ||| ||||| |||||
Db      4257 TTTATGAATGACAGTAGTCACACATAGTGCTGTTTATATAGTTTAGGAGTAAGAGTCTTG 4316
Qy      5112 TGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGG--ATAATAACAGCAGT 5169
      | ||||| ||||| ||||| ||||| ||||| ||||| ||| | |||||
Db      4317 TTTTTTATTTCAGATTGGGAAATCCATTCCATTTTGTGAATTGGGACATAGTTACAGCAGT 4376
Qy      5170 GGAATAAGTACTTA-GAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAA 5228
      ||||| || | | ||||| ||||| ||||| |||
Db      4377 GGAATAAGTATTCATTTAGAAATGTGAATGAGCAGTAAACTGATGAGA-----TAA 4428
Qy      5229 AGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAA--TTTTT 5286
      ||||| ||||| | ||||| ||||| ||||| ||||| ||||| |||||
Db      4429 AGAAATTAAGAGATATTTAATTCTTGCCTTATA-CTCAGTCTATTCGGTAAATTTTTTT 4487
Qy      5287 AAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATC 5346
      | | || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4488 TTAAAAATGTGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGACAAATTAAATC 4547
Qy      5347 TGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCT 5406
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4548 TGAATAAATCATTCTCCCTGTTCACTGGCTCATTTATTCTCTATGCACTGAGCATTTGCT 4607
Qy      5407 TTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCC 5466
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4608 CTGTGGAAGGCCCTGGGTTAATAGTGGAGATGCTAAGGTAAGCCAGACTCACCCCTACCC 4667
Qy      5467 ATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAA 5526
      | ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4668 ACAGGGTAGTAAAGTCTAGGAGCAGCAGTCATATAATTAAGGTGGAGAGATGCCCTCTAA 4727

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RESULT 10

ABQ76205

ID ABQ76205 standard; DNA; 4741 BP.

XX

AC ABQ76205;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human tumour antigen MAGE-5a DNA.

XX

KW Tumour antigen; human; vaccine; cellular immune response; immunogen;

KW cancer; tumour; MAGE-5a; ds.

XX

OS Homo sapiens.

XX

PN US6287569-B1.

XX

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PD 11-SEP-2001.
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XX
PF 06-APR-1998; 98US-00056105.
XX
XX
PR 10-APR-1997; 97US-0043467P.
XX
XX
PA (REGC ) UNIV CALIFORNIA.
XX
XX
PI Kipps TJ, Wu Y;
XX
XX
DR WPI; 1998-583198/49.
XX
XX
PT Generating cellular immune response in patient to target protein -
PT comprises introducing vector with nucleotide sequence encoding immunogen
PT comprising protein processing signal into cell of patient.
XX
XX
PS Disclosure; Col 49-54; 61pp; English.
XX
XX
CC This invention describes a novel method for generating a cellular immune
CC response in a patient to a target protein or its fragment. The method
CC involves introducing a vector containing a nucleotide sequence encoding a
CC chimeric immunogen comprising a protein processing signal and the target
CC protein or its fragment. The immunogen is produced by the cells and
CC processed so that the target protein or its fragment is presented to the
CC patients immune system and a cellular immune response is initiated. The
CC method and vectors can be used as a form of vaccination and could be used
CC to generate a cellular immune response in patients to, e.g. cancerous
CC tumours. The cellular immune response is the predominant immune response
CC in the patient. This sequence represents a DNA fragment which encodes the
CC human tumour antigen MAGE-5a described in the method of the invention.
CC Note: The information in this spec has been previously disclosed in
CC WO199845444 however this spec contained no sequence information
XX
XX
SQ Sequence 4741 BP; 1118 A; 1274 C; 1305 G; 1044 T; 0 U; 0 Other;

Query Match 42.7%; Score 2422.8; DB 2; Length 4741;
Best Local Similarity 75.7%; Pred. No. 0;
Matches 3726; Conservative 0; Mismatches 882; Indels 314; Gaps 46;

Qy 715 TTCCCGCCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGG 774
   ||| ||||| || | ||||| || ||||| ||||| ||||| ||| ||
Db 15 TTCAACCCAGGGAATCCCTGGGTGACCAGATGTGGTGCCACTGTCTTGACATTTGAGGT 74

Qy 775 CAGAGAGAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGA 834
   | ||||| ||| | || ||||| || ||||| || || || || || ||
Db 75 CGGAGAGAAGCAAGGGCCTCGCTCTCAGGGGCAGC-TGGAGATCAGCTGAGGGCAGCTGG 133

Qy 835 CCCAGGCTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTC 894
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||| ||
Db 134 CCCTGGCTCTGTGAGGATGCAAGGTGAGATGCTGAGGGAGGACTAAGGAGTATCCACCC 193

Qy 895 CAAATAGAGAGCCCCAAATATTCCAG---CCCCGCCCTTGCTGCCAGCCCTGGCCCCACCC 951
   | ||| | ||||| ||||| | || | ||||| ||| ||||| ||| ||
Db 194 CTGGTAGTGGACCCCAAATAATCCAGTGCCACCTCTCCTGCTGCTAGCTCTGGACCATCC 253

Qy 952 GCGGGAAGACGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGAC 1011
   || | ||| ||| || ||||| ||||| ||||| || | ||||| || ||
Db 254 AGGGCAGGACTTCTTAGGCTGGGCCACCCCGAGTCCCCACCGCTTAAGCCGAGGGGA- 312

Qy 1012 ACCAGGTTCTTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGT 1071
   ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db      313 -----CTCAGGAGACAGAGCTTGGTATGACCAGGGCAGGACTGGT 352
Qy      1072 TAGGAGAGGGCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGC 1131
      ||||| ||| | || ||||| ||| | ||| | ||| |
Db      353 TAGGAGAGGACAGCTCCCA-GCTCTGCCAGGAAACAACGTCAGGAACCTAAGGGAAAGCT 411
Qy      1132 TGTGGGCCCCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCTATTCCT 1191
      | |||
Db      412 GAGGCTACCCC----- 422
Qy      1192 CACCCAACCCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCAC 1251
      ||||| ||| | ||| ||| ||||| | |
Db      423 -----CACCCAAACTCTATTCTGTCCCTACCTCCGTCC 457
Qy      1252 CTGACCACCACCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCCTCACT 1311
      | ||| ||||| ||| || || ||||| ||| ||||| |||
Db      458 CCCACCTACACCCCATTC-----CCACCCCTTCCCTACCGGCACCTCTATCCACA 512
Qy      1312 GCCCCAACCCACCTCATCTCTCTCATGTGCCCACTCCCATCGCCTCCCCATTCTG 1371
      ||||| ||||| |||
Db      513 TCCCCA-----CCCCTATCCTG 530
Qy      1372 GCAGAATCCGGTT-TGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCGATGTGAA 1430
      ||||| ||| || ||||| ||||| ||||| ||||| ||||| |||||
Db      531 GCAGAATCCGATTCTGCCCTGATTTCAACCCAGGGAAGCCCTAGGGGGCCGGATGTGAT 590
Qy      1431 ACCACTGACTTGAACCTCACAGATCTGAGAGAAGCCAGGTTCAATTAATGGTTCTGAGGG 1490
      | ||||| ||| | || ||||| ||| ||||| |||||
Db      591 GCTGCTGACTTGTGCATTGGGGGTCAGAGAGAATCAAG-----GCATGGTTCTGAGAA 644
Qy      1491 GCGGCTTGAGATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATG 1550
      || | ||||| | ||||| ||| ||||| ||||| ||||| |||||
Db      645 GCCGACTGAGATCAGCAGAGGGGAATGGGCCCGGGCTCTGTGAGGAGGCAAGGTGAGACC 704
Qy      1551 CT-GAGGGAGGACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTAC 1609
      | |||| |||| ||||| || | |||| | | ||| ||||| |||||
Db      705 CCCGAGGAAGGAATGAGGAAGCCCTCACCC--AGATAGAGAACCCCAAATAATCCAGTAC 762
Qy      1610 CACCCCTGCTGCCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCC 1669
      ||| ||||| ||||| ||||| ||||| ||||| ||| |||
Db      763 TACCTTTGCTGCCAGCCCTGGACCAC----CCAGGGCAGACTTCTCAGGCTGAACCTTCC 818
Qy      1670 CCGTCCCGTCCCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTT-ATGTGAC 1728
      | ||| ||||| ||||| ||||| ||| ||| ||||| ||| |||||
Db      819 C---CCCTCCCCTGCCACTTAAGCCACAAGGGACTCTGGAGTCAGACCTTGGTGTGAC 875
Qy      1729 CGGGGCAGGGTTGGTCAGGAGAGGCAGGGGCCAGGCATCAAGGTCCAGCATCCGCCCCGGC 1788
      | ||| |||| ||||| ||||| ||||| ||||| ||| |||
Db      876 CAGGGAAGGGCCGGTCAGGAGAGG-----GCAGGGGCCAGGCTCTGTGAGGC 922
Qy      1789 ATTAGGGTCAGGACCTGGGAGGGAAGTGAAGGTTCCCCACCCACACCTGTCTCCTCATC 1848
      || | ||||| ||||| ||| ||||| ||| ||||| ||| |||
Db      923 ATCAAAATCAGGACCTGAGAGAGAATTGAGGGCCCCACCCCAACCCCTATACCCATCC 982
Qy      1849 TCCACCGCCACCCCACTCACATTCCCATACCTACC----CCCTACCCCAACCTCATCTT 1904
      ||| | ||||| || | ||| || ||||| ||| ||| |||||
Db      983 CTAACCCCATACCCACTCTACTTGCAATTCAGCCCCATCCCCACACCTACCCATCTT 1042
Qy      1905 GTCAGAA-----TCCCTGCTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGG 1954
      | |||| ||||| ||||| ||||| ||||| ||| |||||
Db      1043 GGCAGAATCTGTTTCTTCCCTGCAGTCAACCCACAGAAGCCCCAGGAATGACAGACAGG 1102

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Qy      1955 CACTCGGATCTTGACGTCCCCATCCAGGGTCTGATGGAGGGAAGGG-----GCTTGAA 2007
      ||| |  ||  ||||| ||||| ||||| ||||| ||||| |||||
Db      1103 CACACCTATTCTGACGTCCACATCCAGGGCTGAAGGAGGGAAGGGCTTAGTATCATGAG 1162

Qy      2008 CAGGGCCTCAGGGGAGCAGAGG----GAGGGCCCTACTGCGAGATGAGGGAGGCCTCAGA 2063
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1163 CAGGGCCTCAGGGGAGTCTCTGCTCCTCAAGCCCTGCTGGGAGTAAAGGGAGGCCTCAGG 1222

Qy      2064 GGACCCAGCACCCCTAGGA-----CACCGCACCCCTGTCTGAGACTGAG--GCTGCC 2112
      | ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db      1223 GAACCCAGGTCTCTCAGGATAGGGGGTCCACTCCAACCTGTCTGAGACTGAGGCGCCTCC 1282

Qy      2113 ACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGGGTGGGACCCAGG 2172
      |||  |||  ||||| | ||||| ||||| | ||||| |||||
Db      1283 TCTTTCATCCTCGGAATCAGAGGATGGAGACTCACGTCAGCAGAGGGTGGGGCCCAAC 1342

Qy      2173 CCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTTGAATCCAGATC 2232
      ||||| ||| | | | ||||| ||||| ||||| ||||| ||||| |
Db      1343 CCTGCCAGGATCAAGGAGAGGAAGAAGAGGGAGGACTCAGGGTACCTTTGAGTCCAGAAC 1402

Qy      2233 AGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATGGCCCATATTTCC 2292
      | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Db      1403 AATGGGGACCTTTGCCCTGGGAGGTCCAGTGCACAGTGGCCACCTGTAGCCCATGCTTGC 1462

Qy      2293 TGCATCTTTGAGGTGAC----AGGACAGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTCA 2348
      |||| |||  |||||  |||| | ||||| ||||| ||| ||||| |||||
Db      1463 TGCACCTTCTGGGTGACAAAGAGGAGAGGGCTGTGGTCTAGAGCAGTGGTGACTCAGGTCA 1522

Qy      2349 ACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATGAGGACTGG 2408
      ||||| ||||| |||| |||  | | ||||| ||||| ||||| || |||
Db      1523 GCAGAGGGAGGAGTCCAGCATCTGCAGGCCCAATGTGTGCCCCATTCATGAAGATTGG 1582

Qy      2409 GGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTTTTAGTAGC 2468
      ||||| ||  ||||| ||||| ||||| ||||| ||||| ||||| || |||
Db      1583 GGATA-CCTTGGCTCAGAAAGAAGGGACCCACAGAGTCTGGCTGTCCCCTGATTTTGC 1641

Qy      2469 TCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCACAGGCAGG 2528
      ||  ||||| |||| |||| || ||||| ||| |||| ||||| ||||| |
Db      1642 TCAGAGGGGACCAAATCAAGGATAGCCCTATGTGCCAACCTCATTTGTGCCACAGGAAAG 1701

Qy      2529 AAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCTACTCATGT 2588
      ||||| | ||||| ||||| ||||| ||||| ||||| || ||||| |||
Db      1702 AAGTTGAAGACCCCTCAGGGTGATGGGGTCTTGCAGTAAAGGGGAGCTATCTGCTCATCT 1761

Qy      2589 CAGGGAATTGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGTGAGACAGA 2648
      ||||| ||  ||||| ||||| ||||| | ||| || ||| ||| |||
Db      1762 CAGGGGGTTTCAGGTTGAGGAATGGCAGGCCCATCACGATGAAGAGTAACCCACAGG-- 1819

Qy      2649 CAAGGCTATTGGAATCCACACCCCAAGAAAGGGGTACGCCCTGGACACCTCA----- 2703
      || || | || | ||||| ||||| ||||| ||||| ||||| |||||
Db      1820 ---AGCCATAGAAACACTCACCCCAAGAAAGGGGTACACCTGGACACCCCATGTGG 1876

Qy      2704 ----CCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACC 2759
      ||||| || || | ||| ||||| ||||| ||||| ||||| |||||
Db      1877 GGGTGACAGGATGTAGC-TCCATCTCATTCCTGTTTTCAGATCTCGGGGAGGTGAGGAAC 1935

Qy      2760 TCATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGC 2819
      | ||||| |||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1936 TTGTTCTCCGAGGATGACTCAGGTCAACACAGGGGCCCCCATCTGGTGGATAGACAGAGT 1995

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Qy	2820	GGTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCCCA	2879
Db	1996	GGTCCCAGGATCTGTCTAGTAGTTCCGGTGAGGAACATGAGGGACGATTGAGGGCACCCCTT	2055
Qy	2880	GGACCAGAACACTGAGGGGAGACTGCACAGAAATCAGCCCTGCCCCCTGCTGTACCCCCAGA	2939
Db	2056	GGGCCAGAACACAGATGAGGACCTCACGGAAATCTGCCCTGCCCCCTGCTGTCTACTCCAGA	2115
Qy	2940	GAGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCC--GTTATCCTGGGATCATTGATGTCA	2997
Db	2116	GAGCATGGGCAGGGCTGTCTGCTGCAGTCCCCCCCCACTTACCCTGGGATCATTGGTGTCA	2175
Qy	2998	GGGACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCAG	3057
Db	2176	GGGATGGGGAGGTCTTTGTCTC--GAGGGGTCTGCACTCAGGTCAGTAGAGGGAGCGTCTTAG	2234
Qy	3058	GCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCC	3117
Db	2235	GCCCTGCCAGGAGACAAGGTAAGAACGAAGCAGGTTCTCACCCAGGACACATGAATTCC	2294
Qy	3118	AATGAATTTTGATATCTCTTGCTGCCCTTCCCCA-AGGACCTAGGCACGTGTGGCCAGAT	3176
Db	2295	AATGCATTTTCAGCATCTCTTCCTGTCTTCCCAAGAGGACCTGGGCACGTGTGGCCAGAT	2354
Qy	3177	GTTTGTCCCTCTCTGTCTTCCATTCTTATCATGGATGTGAACCTTGATTGTGGATTTC	3236
Db	2355	GTGAGTCTCCTCATGTCTCT---GTTCCCTATCAGGGATGTGAGCTCTTAATCTGAGTTTC	2411
Qy	3237	TCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTG	3296
Db	2412	TCAGGCCAGCAAAAGGGTGGGATCCAGGCCCTTGCCAGGAGAAAGGTGAGGGCCCTGTGTG	2471
Qy	3297	AGAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCT	3356
Db	2472	AGCACAGAGGGGACCATTACCCCAAGAGGGTGGAGACCTCACAGATTCCAGCCTACCT	2531
Qy	3357	CCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCTGAGGGCCCGTGGAT	3416
Db	2532	CCTGTTAGCACTGGGGCCCTGAGGCTGTGCTTGCACTCTGCACCTGAGGGCCCATGCAT	2591
Qy	3417	TCCTCTTCTCGAGCTCCAGGAACAGGCAGTGAGGCCTTGGTCTGAGACAGTATCTCTCA	3476
Db	2592	TCCTCTTCCAGGAGCTCCAGGAACAGACACTGAGGCCTTGGTCTGAGGCCGTGCCCTCA	2651
Qy	3477	GGTCACAGAGCAGAGGATGCACAGGGT----GTGCCAGCAGTGAATGTTTGCCCTGAATG	3532
Db	2652	GGTCACAGAGCAGAGGAGATGCAGACGTCTAGTGCCAGCAGTGAACGTTTGCCCTGAATG	2711
Qy	3533	CACACCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCA-CC	3591
Db	2712	CACACTAATGGCCCCCATCGCCCCAGAACATATGGGACTCCAGAGCACCTGGCCTCACCC	2771
Qy	3592	TCCCTACTGTCTAGTCTCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCTGAGTACCCTC	3651
Db	2772	TCTCTACTGTCTAGTCTCTGCAGAATCAGCCTCTGCTTGCTTGTGTACCTGAGGTGCCCTC	2831
Qy	3652	TCACTTCCTCCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGAC-----A	3698
Db	2832	TCACTTTTTCTTCAGGTTCTCAGGGGACAGGCTGACCAGGATCACAGGAAGCTCCAGA	2891
Qy	3699	GGATTCCCTGGAGGCCACAGAGGAGCACC-AAGGAGAAGATCTGTAAGTAGGCCTTTGTT	3757



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      |||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2892 GGATCCCCAGGAGGCCCTAGAGGAGCACCAAAGGAGAAGATCTGTAAGTAAGCCTTTGTT 2951

Qy      3758 AGAGTCTCCAAGGTTCACTTCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGC 3817
      |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2952 AGAGCCTCCAAGGTTCACTTTTAGCTGAGGCTTCTCACATGCTCCCTCTCTCCAGGC 3011

Qy      3818 CTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTC 3877
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3012 CAGTGGGTCTCCATTGCCCAGCTCCTGCCCACACTCCTGCCTGTTGCGGTGACCAGAGTC 3071

Qy      3878 ATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAA 3937
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3072 GTCATGTCTCTTGAGCAGAAGAGTCAGCACTGCAAGCCTGAGGAAGGCCTTGACACCCAA 3131

Qy      3938 CAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC-----C 3976
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3132 GAAGAGGCCCTGGGCCTGGTGGGTGTGCAGGCTGCCACTACTGAGGAGCAGGAGGCTGTG 3191

Qy      3977 TCCTCCTCCTCTCCTCTGGTCCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACA 4036
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3192 TCCTCCTCCTCTCCTCTGGTCCCAGGCACCCTGGGGGAGGTGCCCTGCTGCTGGGTACCA 3251

Qy      4037 GATCCTCCCCAGAGTCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGA 4096
      | |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3252 GGTCTCTCAAGAGTCTCAGGGAGCCTCCGCCATCCCCACTGCCATCGATTTCACCTCTA 3311

Qy      4097 CAGAGGCAACCCAGTGAGGGTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGT 4156
      ||||| ||| | |||| ||||| || ||||| ||||| ||||| |||||
Db      3312 TGGAGGCAATCCATTAAAGGGCTCCAGCAACCAAGAAGAGGAGGGGCCAAGCACCTCCCCCT 3371

Qy      4157 ATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTT 4216
      || |||| ||||| ||||| || ||||| ||||| ||||| ||||| |||||
Db      3372 GACCCAGAGTCGTGTTCGAGCAGCACTCAGTAAGAAGGTGGCTGACTTGATTCAATTT 3431

Qy      4217 CTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTC 4276
      ||||| |||| || || |||| ||||| ||||| ||||| ||||| |||||
Db      3432 CTGCTCCTCAAGTATTAAGTCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGAGCGTC 3491

Qy      4277 ATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA 4336
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3492 ATCAAAAATTACAAGCGCTGCTTTCTGAGATCTTCGGCAAAGCCTCCGAGTCCTTGCA 3551

Qy      4337 CTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGTC 4396
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3552 CTGGTCTTTGGCATTGACGTGAAGGAAGCGGACCCACAGCAACACCTACACCCTTGTC 3611

Qy      4397 ACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTG---ATAATCAGATCATGCCCAAG 4453
      ||||| || ||||| ||||| ||||| || ||||| ||||| ||||| |||||
Db      3612 ACCTGCCTGGG--ACTCCTATGATGGCCTGCTGGTTGATAATAATCAGATCATGCCCAAG 3669

Qy      4454 ACAGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAG 4513
      || ||| ||||| |||| |||| ||||| ||||| ||||| ||||| |||||
Db      3670 ACGGGCCTCCTGATAATCGTCTTGGGCATGATTGCAATGGAGGGCAAATGCGTCCCTGAG 3729

Qy      4514 GAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCC 4573
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3730 GAGAAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGTATGTTGGGAGGGAGCACAGTGTC 3789

Qy      4574 TATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA- 4632
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 3790 TGTGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAC TACCTGGAGTAC 3849

Qy 4633 CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTC 4692  
 ||||| ||||| | ||||| ||||| |||||

Db 3850 CGGCAGGTGCCAGCAGTGATCCCATATGCTATGAGTTACTGTGGGGTCCAAGGGCACTC 3909

Qy 4693 GCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTTCGC 4752  
 |||| | ||||| || ||| | ||| ||| ||||| ||||| |

Db 3910 GCTGCT-----TGAAAGTACTGGAGCACGTGGTCAGGGTCAATGCAAGAGTTCTC 3959

Qy 4753 TTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCA 4812  
 ||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 3960 ATTTCTTACCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCA 4019

Qy 4813 TGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGT 4872  
 |||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 4020 TGAGCTGCAGCCAGGGCCACTGCGAGGGGGGCTGGGCCAGTGCACCTTCCAGGGCTCCGT 4079

Qy 4873 CCAGCAGCTTCCCCTGCC--TCGTGTGACATGAGGCCATTCTTCACTC--TGAAGAGAGC 4929  
 |||| || ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 4080 CCAGTAGTTTCCCCTGCCCTAATGTGACATGAGGCCATTCTTCTCTCTTTGAAGAGAGC 4139

Qy 4930 GGTCACTGTTCTCAGTAGAGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGT 4989  
 |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 4140 AGTCAACATTCTTAGTAGTGGGTTTCTGTTCTATTGGATGACTTTGAGATTTGTCTTTGT 4199

Qy 4990 TCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATC 5049  
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 4200 TTCCTTTTGGGAATTGTTCAAATG-TTTCTTTTAATGGGTGGTTGAATGAACCTCAGCATT 4258

Qy 5050 CAAGTTTATGAATGACAGCAGTCACAC--AGTTCTGTGTATATAGTTTAAGGGTAAGAGT 5107  
 ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 4259 CAAATTTATGAATGACAGTAGTCACACATAGTGCTGTTTATATAGTTTAGGAGTAAGAGT 4318

Qy 5108 CTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGG--ATAATAACAG 5165  
 |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 4319 CTTGTTTTTTATTTCAGATTGGGAAATCCATTCCATTTTGTGAATTGGGACATAGTTACAG 4378

Qy 5166 CAGTGGAAATAAGTACTTA-GAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAA 5224  
 ||||| ||||| ||| | ||||| ||||| ||||| ||||| |||||

Db 4379 CAGTGGAAATAAGTATTCATTTAGAAATGTGAATGAGCAGTAAACTGATGACA----- 4431

Qy 5225 CTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAATTT 5284  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 4432 -TAAAGAAATTAAGAGATATTTAATTCTTGCTTATACTCAGTCTATTCGGTAAATTTTT 4490

Qy 5285 TTAAAGATATATGCATACCTGGATTTCTTGCCCTTATACCTCAGTCTATTCTGTAAATTT 5344  
 || || | || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 4491 TTTAAAAAATGTGCATACCTGGATTTCTTGCCCTTCTTTGAGAATGTAAGACAAATTA 4550

Qy 5345 TCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTG 5404  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 4551 TCTGAATAAATCATTCTCCCTGTTCACTGGCTCATTTATTCTCTATGCACTGAGCATTTG 4610

Qy 5405 CTTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCAC 5464  
 || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 4611 CTCTGTGGGAAGGCCCTGGGTTAATAGTGGAGATGCTAAGGTAAGCCAGACTCACCCCTAC 4670

Qy 5465 CCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCT 5524  
 ||| |||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 4671 CCACAGGGTAGTAAAGTCTAGGAGCAGCAGTCATATAATTAAGGTGGAGAGATGCCCTCT 4730

Qy 5525 AA 5526  
||  
Db 4731 AA 4732

RESULT 11

AAQ32351

ID AAQ32351 standard; DNA; 2419 BP.

XX

AC AAQ32351;

XX

DT 25-MAR-2003 (revised)

DT 22-APR-1993 (first entry)

XX

DE Antigen E gene.

XX

KW Stable; antigen; E; D; F; A; human; melanoma; cell line; MZ2-MEL;

KW cytolytic T cell; MEL3.1; open reading frame; homology; MAGE;

KW melanoma antigen; ss.

XX

OS Homo sapiens.

XX

PN WO9220356-A1.

XX

PD 26-NOV-1992.

XX

PF 22-MAY-1992; 92WO-US004354.

XX

PR 23-MAY-1991; 91US-00705702.

PR 09-JUL-1991; 91US-00728838.

PR 23-SEP-1991; 91US-00764364.

PR 12-DEC-1991; 91US-00807043.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Boon T, Van Der Bruggen P, Van Den Eynde B, Van Pel A, De Plaen E;

PI Lurquin C, Chomez P, Traversari C;

XX

DR WPI; 1992-415460/50.

XX

PT Nucleic acid mol. encoding a human tumour rejection antigen precursor -

PT useful as an immunostimulant in a vaccine for treating and preventing

PT cancers, also useful in diagnosis.

XX

PS Disclosure; Page 69-70; 142pp; English.

XX

CC This sequence encodes the stable antigen E. This antigen is expressed  
CC along with antigens "D, F and A" by the human melanoma cell line MZ2-  
CC MEL. These antigens are all recognised by cytolytic T cells. A subline of  
CC MZ2-MEL is MEL3.1 which only expresses antigen E. This cell line was  
CC chosen as a source for the isolation of this sequence. This sequence was  
CC found to contain three exons. The open reading frame for antigen E was  
CC contained within the first two exons. An ATG is located at position 66 of  
CC exon 3 and is followed by an 828 base pair reading frame. The three exons  
CC contain 65, 73 and 1551 base pairs. During the isolation of this sequence  
CC two different but closely related cDNAs were also identified. These cDNAs,  
CC when tested, did not transfer expression of antigen E, but they did show  
CC substantial homology to the antigen E cDNA sequence. These new cDNAs  
CC represent a new family of genes referred to as melanoma antigens (MAGE)  
CC (see also AAQ32352-69). (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 2419 BP; 562 A; 581 C; 677 G; 599 T; 0 U; 0 Other;

Query Match 42.6%; Score 2419; DB 2; Length 2419;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2419; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
          |||
Db       1  GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

QY      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          |||
Db      61  ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

QY      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA 3435
          |||
Db     121  CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA 180

QY      3436 GGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          |||
Db     181  GGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

QY      3496 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          |||
Db     241  CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

QY      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCTGTAGAAT 3615
          |||
Db     301  CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCTGTAGAAT 360

QY      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 3675
          |||
Db     361  CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 420

QY      3676 GGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAGGAGAA 3735
          |||
Db     421  GGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAGGAGAA 480

QY      3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCCTCTCA 3795
          |||
Db     481  GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCCTCTCA 540

QY      3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCTCCTGCCACACTCCT 3855
          |||
Db     541  CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCTCCTGCCACACTCCT 600

QY      3856 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 3915
          |||
Db     601  GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 660

QY      3916 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 3975
          |||
Db     661  TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 720

QY      3976 CTCCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCCACTGCTGGGTCAAC 4035
          |||
Db     721  CTCCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCCACTGCTGGGTCAAC 780

QY      4036 AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG 4095
          |||
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Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGG	4635
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGG	1380
Qy	4636	CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGCT	4695
Db	1381	CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGCT	1440
Qy	4696	GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTTCGCTTT	4755
Db	1441	GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTTCGCTTT	1500
Qy	4756	TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA	4815
Db	1501	TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA	1560
Qy	4816	GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCA	4875
Db	1561	GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCA	1620
Qy	4876	GCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCAG	4935
Db	1621	GCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCAG	1680
Qy	4936	TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT	4995
Db	1681	TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT	1740

Qy	4996	TTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTT	5055
Db	1741	TTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTT	1800
Qy	5056	TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTT	5115
Db	1801	TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTT	1860
Qy	5116	TTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAATA	5175
Db	1861	TTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAATA	1920
Qy	5176	AGTACTTAGAAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT	5235
Db	1921	AGTACTTAGAAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT	1980
Qy	5236	AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTTAAAGATATA	5295
Db	1981	AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTTAAAGATATA	2040
Qy	5296	TGCATACCTGGATTTCCTTGCCCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAG	5355
Db	2041	TGCATACCTGGATTTCCTTGCCCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAG	2100
Qy	5356	AATTCTTCCTGTTCACCTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTTGAAG	5415
Db	2101	AATTCTTCCTGTTCACCTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTTGAAG	2160
Qy	5416	GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG	5475
Db	2161	GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG	2220
Qy	5476	TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG	5535
Db	2221	TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG	2280
Qy	5536	GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGC	5595
Db	2281	GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGC	2340
Qy	5596	CCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTGT	5655
Db	2341	CCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTGT	2400
Qy	5656	AATGATCTTGGGTGGATCC	5674
Db	2401	AATGATCTTGGGTGGATCC	2419

RESULT 12

AAQ72476

ID AAQ72476 standard; DNA; 2419 BP.

XX

AC AAQ72476;

XX

DT 25-MAR-2003 (revised)

DT 21-JUN-1995 (first entry)

XX

DE Tumour rejection antigen E encoding DNA.

XX

KW Tumour rejection antigen E; melanoma antigen-3; MAGE-3; cancer;  
KW cytolytic T cells; antigen D; human leucocyte antigen; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9423031-A1.  
XX  
PD 13-OCT-1994.  
XX  
PF 17-MAR-1994; 94WO-US002877.  
XX  
PR 26-MAR-1993; 93US-00037230.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
XX  
PI Gaugler B, Van Den Eynde B, Boon-Falleur T, Van Der Bruggen P;  
XX  
DR WPI; 1994-333192/41.  
XX  
PT New tumour rejection antigen precursor MAGE3 - useful in treatment and  
PT diagnosis of cancer.  
XX  
PS Disclosure; Page 58; 105pp; English.  
XX  
CC AAQ72476 encodes tumour rejection antigen E, another sequence AAQ72470  
CC encodes melanoma antigen-3 (MAGE-3) a tumour rejection antigen precursor.  
CC Melanomas characterised by the expression of MAGE-3 can be detected, or  
CC monitored, by contacting a test sample with an agent that can recognise  
CC MAGE-3. The melanoma can be treated by the administration of cytolytic T  
CC cells specific for the complex of antigen D (the mature rejection antigen  
CC derived from MAGE-3) and a human leucocyte antigen (esp. HLA-A1).  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 2419 BP; 562 A; 581 C; 677 G; 599 T; 0 U; 0 Other;

Qy	3256	GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC	3315
Db	1	GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC	60
Qy	3316	ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTGGTAGCACTGAGAAGC	3375
Db	61	ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTGGTAGCACTGAGAAGC	120
Qy	3376	CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGGAGCTCCA	3435
Db	121	CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGGAGCTCCA	180
Qy	3436	GGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG	3495
Db	181	GGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG	240
Qy	3496	CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA	3555
Db	241	CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA	300
Qy	3556	CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTGTCAGTCTGTAGAAT	3615

Db 301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCCTGTAGAAT 360

Qy 3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 3675  
 |||

Db 361 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 420

Qy 3676 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 3735  
 |||

Db 421 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 480

Qy 3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 3795  
 |||

Db 481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 540

Qy 3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT 3855  
 |||

Db 541 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT 600

Qy 3856 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 3915  
 |||

Db 601 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 660

Qy 3916 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 3975  
 |||

Db 661 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 720

Qy 3976 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 4035  
 |||

Db 721 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 780

Qy 4036 AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG 4095  
 |||

Db 781 AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG 840

Qy 4096 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG 4155  
 |||

Db 841 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG 900

Qy 4156 TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT 4215  
 |||

Db 901 TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT 960

Qy 4216 TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT 4275  
 |||

Db 961 TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT 1020

Qy 4276 CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA 4335  
 |||

Db 1021 CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA 1080

Qy 4336 GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT 4395  
 |||

Db 1081 GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT 1140

Qy 4396 CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC 4455  
 |||

Db 1141 CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC 1200

Qy 4456 AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA 4515  
 |||

Db 1201 AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA 1260



Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGG	4635
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGG	1380
Qy	4636	CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT	4695
Db	1381	CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT	1440
Qy	4696	GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT	4755
Db	1441	GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT	1500
Qy	4756	TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA	4815
Db	1501	TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA	1560
Qy	4816	GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCA	4875
Db	1561	GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCA	1620
Qy	4876	GCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCAG	4935
Db	1621	GCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCAG	1680
Qy	4936	TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT	4995
Db	1681	TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT	1740
Qy	4996	TTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGTT	5055
Db	1741	TTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGTT	1800
Qy	5056	TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTT	5115
Db	1801	TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTT	1860
Qy	5116	TTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGGAATA	5175
Db	1861	TTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGGAATA	1920
Qy	5176	AGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT	5235
Db	1921	AGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT	1980
Qy	5236	AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATA	5295
Db	1981	AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATA	2040
Qy	5296	TGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAG	5355
Db	2041	TGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAG	2100
Qy	5356	AATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAAG	5415
Db	2101	AATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAAG	2160

Qy 5416 GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG 5475  
 |||  
 Db 2161 GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG 2220

Qy 5476 TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG 5535  
 |||  
 Db 2221 TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG 2280

Qy 5536 GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGC 5595  
 |||  
 Db 2281 GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGC 2340

Qy 5596 CCTGAGCTGGGGCATTCTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTGT 5655  
 |||  
 Db 2341 CCTGAGCTGGGGCATTCTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTGT 2400

Qy 5656 AATGATCTTGGGTGGATCC 5674  
 |||  
 Db 2401 AATGATCTTGGGTGGATCC 2419

RESULT 13

AAX84112

ID AAX84112 standard; DNA; 2419 BP.

XX

AC AAX84112;

XX

DT 08-SEP-1999 (first entry)

XX

DE Antigen E coding sequence.

XX

KW Tumour rejection antigen; vaccine; cancer; antigen E; ss.

XX

OS Homo sapiens.

XX

PN US5925729-A.

XX

PD 20-JUL-1999.

XX

PF 02-MAY-1994; 94US-00142368.

XX

PR 23-MAY-1991; 91US-00705702.

PR 09-JUL-1991; 91US-00728838.

PR 23-SEP-1991; 91US-00764365.

PR 12-DEC-1991; 91US-00807043.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Van Der Bruggen P, Traversari C, Lurquin C, Boon T, De Plaen E;

PI Van Pel A, Chomez P, Van Den Eynde B;

XX

DR WPI; 1999-418294/35.

XX

PT New tumour rejection antigen is useful as a vaccine against cancerous diseases.

XX

PS Disclosure; Col 37-40; 58pp; English.

XX

CC This sequence represents the antigen E coding sequence. The invention relates to a tumour rejection antigen sequence that is useful as a tumour rejection antigen for vaccination against cancerous conditions

XX

SQL Sequence 2419 BP; 562 A; 581 C; 677 G; 599 T; 0 U; 0 Other;

Query Match 42.6%; Score 2419; DB 2; Length 2419;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2419; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
          |||
Db       1  GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          |||
Db      61  ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA 3435
          |||
Db     121  CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          |||
Db     181  GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          |||
Db     241  CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 3615
          |||
Db     301  CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 360

Qy      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTCAGGTTTTTCAG 3675
          |||
Db     361  CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTCAGGTTTTTCAG 420

Qy      3676 GGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 3735
          |||
Db     421  GGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 480

Qy      3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCCTCAGCTGAGGCCTCTCA 3795
          |||
Db     481  GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCCTCAGCTGAGGCCTCTCA 540

Qy      3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT 3855
          |||
Db     541  CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT 600

Qy      3856 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 3915
          |||
Db     601  GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 660

Qy      3916 TGAGGAAGCCCTTGAGGCCCCAACAAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 3975
          |||
Db     661  TGAGGAAGCCCTTGAGGCCCCAACAAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 720

Qy      3976 CTCCTCTCTCTCTCTGCTGCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 4035
          |||
Db     721  CTCCTCTCTCTCTCTGCTGCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 780

Qy      4036 AGATCCTCCCCAGAGTCCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG 4095
          |||
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Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGG	4635
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGG	1380
Qy	4636	CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCGTGTGGGTCCAAGGGCCCTCGCT	4695
Db	1381	CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCGTGTGGGTCCAAGGGCCCTCGCT	1440
Qy	4696	GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT	4755
Db	1441	GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT	1500
Qy	4756	TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA	4815
Db	1501	TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA	1560
Qy	4816	GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCA	4875
Db	1561	GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCA	1620
Qy	4876	GCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCAG	4935
Db	1621	GCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCAG	1680
Qy	4936	TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT	4995
Db	1681	TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT	1740

Qy	4996	TTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTT	5055
Db	1741	TTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTT	1800
Qy	5056	TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTT	5115
Db	1801	TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTT	1860
Qy	5116	TTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGGAATA	5175
Db	1861	TTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGGAATA	1920
Qy	5176	AGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT	5235
Db	1921	AGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT	1980
Qy	5236	AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATA	5295
Db	1981	AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATA	2040
Qy	5296	TGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAG	5355
Db	2041	TGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAG	2100
Qy	5356	AATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGGAAG	5415
Db	2101	AATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGGAAG	2160
Qy	5416	GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG	5475
Db	2161	GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG	2220
Qy	5476	TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG	5535
Db	2221	TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG	2280
Qy	5536	GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGC	5595
Db	2281	GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGC	2340
Qy	5596	CCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTGT	5655
Db	2341	CCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTGT	2400
Qy	5656	AATGATCTTGGGTGGATCC	5674
Db	2401	AATGATCTTGGGTGGATCC	2419

RESULT 14

AAT05086

ID AAT05086 standard; DNA; 2419 BP.

XX

AC AAT05086;

XX

DT 25-MAR-2003 (revised)

DT 26-FEB-1996 (first entry)

XX

DE MZ2-MEL antigen E precursor gene.

XX

KW Melanoma; MZ2-MEL; tumour rejection antigen; cancer; diagnosis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9523874-A1.  
 XX  
 PD 08-SEP-1995.  
 XX  
 PF 23-FEB-1995; 95WO-US002203.  
 XX  
 PR 01-MAR-1994; 94US-00204727.  
 PR 10-MAR-1994; 94US-00209172.  
 PR 01-SEP-1994; 94US-00299849.  
 PR 30-NOV-1994; 94US-00346774.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI De Plaen E, Boon-Falleur T, Lethe B, Szikora J, De Smet C;  
 PI Chomez P, Gaugler B, Van Den Eynde B, Brasseur F, Patard J;  
 PI Weynants P, Marchand M, Van Der Bruggen P;  
 XX  
 DR WPI; 1995-320586/41.  
 XX  
 PT Determn. of cancerous condition(s) - using a nucleic acid as a primer to  
 PT determine expression of a MAGE tumour rejection antigen precursor.  
 XX  
 PS Example 20; Page 69-70; 121pp; English.  
 XX  
 CC A gene sequence (AAT05086) hybridizes with a 2.4 kb fragment from human  
 CC melanoma cell line MZ2-MEL but not with E- antigen loss variants of MZ2-  
 CC MEL. This E precursor antigen gene sequence was obtd. from a cosmid  
 CC derived from DNA of the E+ subclone MZ2-MEL 43. (Updated on 25-MAR-2003  
 CC to correct PI field.)  
 XX  
 SQ Sequence 2419 BP; 560 A; 581 C; 677 G; 601 T; 0 U; 0 Other;

Query Match 42.6%; Score 2415.8; DB 2; Length 2419;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 2417; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60  
 QY 3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTGGTAGCACTGAGAAGC 3375  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTGGTAGCACTGAGAAGC 120  
 QY 3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTCCTGGAGCTCCA 3435  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTCCTGGAGCTCCA 180  
 QY 3436 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240  
 QY 3496 CACAGGGTGTGCCAGCAGTGAATGTTTGGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 CACAGGGTGTGCCAGCAGTGAATGTTTGGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300  
 QY 3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTGTCAGTCCTGTAGAAT 3615

Db	301		CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCTAGTCCCTGTAGAAAT	360
Qy	3616		CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTTCCTTCAGGTTTTTCAG	3675
Db	361		CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTTCCTTCAGGTTTTTCAG	420
Qy	3676		GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAGGAGAA	3735
Db	421		GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAGGAGAA	480
Qy	3736		GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA	3795
Db	481		GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA	540
Qy	3796		CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT	3855
Db	541		CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT	600
Qy	3856		GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	3915
Db	601		GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	660
Qy	3916		TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	3975
Db	661		TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	720
Qy	3976		CTCCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	4035
Db	721		CTCCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	780
Qy	4036		AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	4095
Db	781		AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096		ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841		ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156		TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901		TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216		TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961		TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276		CATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021		CATCATTAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336		GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081		GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396		CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141		CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456		AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515

Db	1201	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAAGTACCTGGAGTACGG	4635
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAAGTACCTGGAGTACGG	1380
Qy	4636	CAGGTGCCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT	4695
Db	1381	CAGGTGCCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT	1440
Qy	4696	GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT	4755
Db	1441	GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT	1500
Qy	4756	TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA	4815
Db	1501	TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA	1560
Qy	4816	GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCAGGGCCGCGTCCA	4875
Db	1561	GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCAGGGCCGCGTCCA	1620
Qy	4876	GCAGCTTCCCTGCGTCGTGTGACATGAGGCCCATTCCTTCACTCTGAAGAGAGCGGTCAG	4935
Db	1621	GCAGCTTCCCTGCGTCGTGTGACATGAGGCCCATTCCTTCACTCTGAAGAGAGCGGTCAG	1680
Qy	4936	TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT	4995
Db	1681	TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT	1740
Qy	4996	TTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGTT	5055
Db	1741	TTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGTT	1800
Qy	5056	TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTT	5115
Db	1801	TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTT	1860
Qy	5116	TTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGGAATA	5175
Db	1861	TTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGGAATA	1920
Qy	5176	AGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT	5235
Db	1921	AGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT	1980
Qy	5236	AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATA	5295
Db	1981	AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATA	2040
Qy	5296	TGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAG	5355
Db	2041	TGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAG	2100
Qy	5356	AATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGGAAG	5415
Db	2101	AATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGGAAG	2160



Qy 5416 GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG 5475  
 |||  
 Db 2161 GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG 2220

Qy 5476 TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG 5535  
 |||  
 Db 2221 TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG 2280

Qy 5536 GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGC 5595  
 |||  
 Db 2281 GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGC 2340

Qy 5596 CCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTGT 5655  
 |||  
 Db 2341 CCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTGT 2400

Qy 5656 AATGATCTTGGGTGGATCC 5674  
 |||  
 Db 2401 AATGATCTTGGGTGGATCC 2419

RESULT 15

AAQ72472

ID AAQ72472 standard; DNA; 2420 BP.

XX

AC AAQ72472;

XX

DT 25-MAR-2003 (revised)

DT 21-JUN-1995 (first entry)

XX

DE Tumour rejection antigen E precursor gene DNA.

XX

KW Tumour antigen rejection precursor E; melanoma antigen-3; MAGE-3; cancer;  
 KW cytolytic T cells; antigen D; human leucocyte antigen; ss.

XX

OS Homo sapiens.

XX

PN WO9423031-A1.

XX

PD 13-OCT-1994.

XX

PF 17-MAR-1994; 94WO-US002877.

XX

PR 26-MAR-1993; 93US-00037230.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Gaugler B, Van Den Eynde B, Boon-Falleur T, Van Der Bruggen P;

XX

DR WPI; 1994-333192/41.

XX

PT New tumour rejection antigen precursor MAGE3 - useful in treatment and  
 PT diagnosis of cancer.

XX

PS Example 20; Page 28; 105pp; English.

XX

CC AAQ72472 is the tumour rejection antigen E precursor gene, another gene

CC AAQ72470 encodes melanoma antigen-3 (MAGE-3) also a tumour rejection

CC antigen precursor. Melanomas characterised by the expression of MAGE-3

CC can be detected, or monitored, by contacting a test sample with an agent

CC that can recognise MAGE-3. The melanoma can be treated by the  
CC administration of cytolytic T cells specific for the complex of antigen D  
CC (the mature rejection antigen derived from MAGE-3) and a human leucocyte  
CC antigen (esp. HLA-A1). (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 2420 BP; 562 A; 582 C; 677 G; 599 T; 0 U; 0 Other;

Query Match 42.4%; Score 2408; DB 2; Length 2420;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
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Db      1 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
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Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGGAGCTCCA 3435
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Qy      3436 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
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Db      181 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

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Qy      3676 GGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 3735
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Db      421 GGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 480

Qy      3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCACTTCTCAGCTGAGGCCTCTCA 3795
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Qy      3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCTCCTGCCCCACACTCCT 3855
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Qy      3916 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 3975
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Db	721	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCTGGAGGAGGTGCCCACTGCTGGGTCAAC	780
Qy	4036	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	4095
Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG	4634
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG	1380
Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	1500
Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814
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Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	1680

Qy	4935	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCT	1740
Qy	4995	TTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT	5054
Db	1741	TTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAA	5174
Db	1861	TTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAA	1920
Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	5294
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Qy	5355	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCAC TGAGCATCTGCTTTTGGAA	5414
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Qy	5415	GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	5474
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Qy	5475	G TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG	5534
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Qy	5535	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGCAATG	5594
Db	2281	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGCAATG	2340
Qy	5595	CCCTGAGCTGGGGCATT TTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTG	5654
Db	2341	CCCTGAGCTGGGGCATT TTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTG	2400
Qy	5655	TAATGATCTTGGGTGGATCC	5674
Db	2401	TAATGATCTTGGGTGGATCC	2420

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Job time : 3217 secs

SCORE 1.3 BuildDate: 12/06/2005
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# SCORE Search Results Details for Application 08819669 and Search Result us-08-819-669e-8.rnpbm.

<a href="#">Score Home Page</a>	<a href="#">Retrieve Application List</a>	<a href="#">SCORE System Overview</a>	<a href="#">SCORE FAQ</a>	<a href="#">Comments / Suggestions</a>
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This page gives you Search Results detail for the Application 08819669 and Search Result us-08-819-669e-8.rnpbm.

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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2006, 12:01:51 ; Search time 6169 Seconds  
(without alignments)  
11301.677 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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	2	2513.6	44.3	4895	6	US-10-102-524-1696	Sequence 1696, Ap
	3	2513.6	44.3	4895	9	US-10-482-029-147	Sequence 147, App
	4	2422.8	42.7	4741	9	US-10-482-029-87	Sequence 87, Appl
	5	2408	42.4	2420	7	US-10-117-937-81	Sequence 81, Appl
	6	2408	42.4	2420	9	US-10-741-466-5	Sequence 5, Appli
	7	2408	42.4	2420	9	US-10-657-022-81	Sequence 81, Appl
	8	2408	42.4	2420	9	US-10-807-308-17	Sequence 17, Appl
	9	2408	42.4	2420	9	US-10-866-484-5	Sequence 5, Appli
	10	2408	42.4	2420	9	US-10-482-029-91	Sequence 91, Appl
	11	2408	42.4	2420	10	US-10-871-708-14	Sequence 14, Appl
	12	2408	42.4	2420	13	US-11-067-064-81	Sequence 81, Appl
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	14	2408	42.4	2420	16	US-11-155-288-25	Sequence 25, Appl
	15	2404.8	42.4	2420	6	US-10-093-766-41	Sequence 41, Appl
	16	2404.8	42.4	2420	6	US-10-116-802-250	Sequence 250, App
c	17	2390.4	42.1	2408	6	US-10-027-632-111713	Sequence 111713,
c	18	2390.4	42.1	2408	6	US-10-027-632-111714	Sequence 111714,
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c	21	2307.6	40.7	302250	3	US-09-962-832-154	Sequence 154, App
c	22	2307.6	40.7	302250	10	US-10-843-641A-6040	Sequence 6040, Ap
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	31	1762.6	31.1	4204	3	US-09-954-456-747	Sequence 747, App
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	33	1762.6	31.1	4204	3	US-09-860-840-1	Sequence 1, Appli
	34	1762.6	31.1	4204	3	US-09-849-602-14	Sequence 14, Appl
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	38	1762.6	31.1	4204	9	US-10-657-022-83	Sequence 83, Appl
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	41	1762.6	31.1	4204	10	US-10-871-708-15	Sequence 15, Appl
	42	1762.6	31.1	4204	13	US-11-067-064-83	Sequence 83, Appl
	43	1762.6	31.1	4204	13	US-11-067-159-83	Sequence 83, Appl
	44	1762.6	31.1	4204	16	US-11-155-288-26	Sequence 26, Appl
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#### ALIGNMENTS

RESULT 1



Db	111572	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCCTCTTCATTGTCATTCCAACCCCC	111513
Qy	600	ACCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCC	659
Db	111512	ACCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCC	111453
Qy	660	TCACCCCCACCCCCACCCCCACGCCCACTCCCACCCCCACCCAGGCAGGATCCGGTTCCC	719
Db	111452	TCACCCCCACCCCCACCCCCACGCCCACTCCCACCCCCACCCAGGCAGGATCCGGTTCCC	111393
Qy	720	GCCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAG	779
Db	111392	GCCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAG	111333
Qy	780	AGAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAG	839
Db	111332	AGAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAG	111273
Qy	840	GCTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAAT	899
Db	111272	GCTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAAT	111213
Qy	900	AGAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGGAAG	959
Db	111212	AGAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGGAAG	111153
Qy	960	ACGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTT	1019
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Qy	1080	GGCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCC	1139
Db	111032	GGCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCC	110973
Qy	1140	CCCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAAC	1199
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Qy	1200	CCCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCAC	1259
Db	110912	CCCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCAC	110853
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Qy	1320	CCCCACCCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATTTCTGGCAGAATC	1379
Db	110792	CCCCACCCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATTTCTGGCAGAATC	110733
Qy	1380	CGGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGAC	1439
Db	110732	CGGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGATGGCCCGATGTGAAACCACTGAC	110673
Qy	1440	TTGAACCTCACAGATCTGAGAGAAGCCAGGTTCAATTAATGGTTCTGAGGGGCGGCTTGA	1499
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Qy	1500	GATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAG	1559
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Qy	1560	GACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCT	1619
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Db	110432	CCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGT	110373
Qy	1740	TGGTCAGGAGA-GGCAGGGCCCAGGCATCAAGGTCCA-GCATCCGCCCGGCATTAGGGTC	1797
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Db	110252	ACCCCACTCACATTCCCATACTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTG	110193
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Qy	1978	CCAGGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCC	2037
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Qy	2038	TACTGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTAGGACACCGCACCCCTGTCT	2097
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Qy	2217	CCTTGGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACA	2276
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Qy	2277	TATGGCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGG	2336
Db	109833	TATGGCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGG	109774
Qy	2337	GGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTT	2396
Db	109773	GGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTT	109714

Qy	2397	CATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCC	2456
Db	109713	CATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCC	109654
Qy	2457	CCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGT	2516
Db	109653	CCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGT	109594
Qy	2517	ACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGAT	2576
Db	109593	ACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGAT	109534
Qy	2577	GTCTACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGAT	2636
Db	109533	GTCTACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGAT	109474
Qy	2637	GAGTGAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTCAGCCCTGGA	2696
Db	109473	GAGTGAGACAGACAAGGCTATTGGAATCCTCACCCCAGAACCAAAGGGGTCAGCCCTGGA	109414
Qy	2697	CACCTCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGG	2756
Db	109413	CACCTCACCCAGGATGTGGCTTC-TTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGG	109355
Qy	2757	ACCTCATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAG	2816
Db	109354	ACCTCATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAG	109295
Qy	2817	AGCGGTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACC	2876
Db	109294	AGCGGTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACC	109235
Qy	2877	CCAGGACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCC	2936
Db	109234	CCAGGACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCC	109175
Qy	2937	AGAGAGCATGGGCTGGGCCGCTGCGGAGGTCCTTCCGTTATCCTGGGATCATTGATGTC	2996
Db	109174	AGAGAGCATGGGCTGGGCCGCTGCGGAGGTCCTTCCGTTATCCTGGGATCATTGATGTC	109115
Qy	2997	AGGGACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCA	3056
Db	109114	AGGGACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCA	109055
Qy	3057	GGCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTC	3116
Db	109054	GGCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTC	108995
Qy	3117	CAATGAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGAT	3176
Db	108994	CAATGAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGAT	108935
Qy	3177	GTTTGTCCCCCTCTGTCCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGATTTC	3236
Db	108934	GTTTGTCCCCCTCTGTCCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGATTTC	108875
Qy	3237	TCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTG	3296
Db	108874	TCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTG	108815
Qy	3297	AGAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCT	3356

Db	108814	AGAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCT	108755
Qy	3357	CCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGAT	3416
Db	108754	CCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGAT	108695
Qy	3417	TCCTCTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCA	3476
Db	108694	TCCTCTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCA	108635
Qy	3477	GGTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACA	3536
Db	108634	GGTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACA	108575
Qy	3537	CCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCT	3596
Db	108574	CCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCT	108515
Qy	3597	ACTGTCAGTCCGTAGAAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACT	3656
Db	108514	ACTGTCAGTCCGTAGAAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACT	108455
Qy	3657	TCCTCCTTCAGGTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCAC	3716
Db	108454	TCCTCCTTCAGGTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCAC	108395
Qy	3717	AGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACT	3776
Db	108394	AGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACT	108335
Qy	3777	TCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCC	3836
Db	108334	TCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCC	108275
Qy	3837	AGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGA	3896
Db	108274	AGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGA	108215
Qy	3897	GGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG	3956
Db	108214	GGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG	108155
Qy	3957	TGTGTGTGCAGGCTGCCACCTCCTCCTCTCTCTGCTTGGTCCCTGGGCACCCCTGGAGGAGG	4016
Db	108154	TGTGTGTGCAGGCTGCCACCTCCTCCTCTCTCTGCTTGGTCCCTGGGCACCCCTGGAGGAGG	108095
Qy	4017	TGCCCCTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCA	4076
Db	108094	TGCCCCTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCA	108035
Qy	4077	CTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGG	4136
Db	108034	CTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGG	107975
Qy	4137	AGGGGCCAAGCACCTCTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGG	4196
Db	107974	AGGGGCCAAGCACCTCTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGG	107915
Qy	4197	TGGCTGATTTGGTTGGTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGG	4256

Db	107914	TGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGG	107855
Qy	4257	CAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCA	4316
Db	107854	CAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCA	107795
Qy	4317	AAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCG	4376
Db	107794	AAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCG	107735
Qy	4377	GCCACTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATA	4436
Db	107734	GCCACTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATA	107675
Qy	4437	ATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGG	4496
Db	107674	ATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGG	107615
Qy	4497	GCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATG	4556
Db	107614	GCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATG	107555
Qy	4557	GGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGG	4616
Db	107554	GGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGG	107495
Qy	4617	AAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGT	4675
Db	107494	AAAAGTACCTGGAGTACCGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGT	107435
Qy	4676	GGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGG	4735
Db	107434	GGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGG	107375
Qy	4736	TCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGG	4795
Db	107374	TCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGG	107315
Qy	4796	AAGAGGGAGTC TGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGC	4855
Db	107314	AAGAGGGAGTC TGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGC	107255
Qy	4856	ACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTC	4915
Db	107254	ACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTC	107195
Qy	4916	ACTCTGAAGAGAGCGGTGAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGG	4975
Db	107194	ACTCTGAAGAGAGCGGTGAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGG	107135
Qy	4976	AGATTTATCTTTGTTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAA	5035
Db	107134	AGATTTATCTTTGTTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAA	107075
Qy	5036	TGAACTTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTT	5095
Db	107074	TGAACTTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTT	107015
Qy	5096	AAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGG	5155
Db	107014	AAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGG	106955

Qy 5156 ATAATAACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGA 5215  
 |||  
 Db 106954 ATAATAACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGA 106895  
 Qy 5216 GATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCT 5275  
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 Db 106894 GATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCT 106835  
 Qy 5276 GTAAAATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGA 5335  
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 Db 106834 GTAAAATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGA 106775  
 Qy 5336 GAAATTAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACT 5395  
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 Db 106774 GAAATTAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACT 106715  
 Qy 5396 GAGCATCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACT 5455  
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 Db 106714 GAGCATCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACT 106655  
 Qy 5456 CATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAG 5515  
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 Db 106654 CATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAG 106595  
 Qy 5516 ATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGA 5575  
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 Db 106594 ATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGA 106535  
 Qy 5576 GAGTGGTGGAGTGTCATGCCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTC 5635  
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 Db 106534 GAGTGGTGGAGTGTCATGCCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTC 106475  
 Qy 5636 CTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674  
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 Db 106474 CTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 106436

RESULT 2

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; Sequence 1696, Application US/10102524

; Publication No. US20030109434A1

; GENERAL INFORMATION:

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Gaiger, Alexander

; APPLICANT: Gordon, Brian

; APPLICANT: Harlocker, Susan L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER

; FILE REFERENCE: 210121.572

; CURRENT APPLICATION NUMBER: US/10/102,524

; CURRENT FILING DATE: 2002-03-19

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; SOFTWARE: FastSEQ for Windows Version 4.0

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; LENGTH: 4895

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-102-524-1696

Query Match 44.3%; Score 2513.6; DB 6; Length 4895;  
 Best Local Similarity 79.9%; Pred. No. 0;  
 Matches 3415; Conservative 0; Mismatches 694; Indels 165; Gaps 32;

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Qy      1478 ATGGTTCTGAGGGGCGGCTTGAGATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAG 1537
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Db      607 ATAGTCCTGAGGGGCCAGTTGAGATCGGCTGAGGGGAGCGGGCCCAAGCTCTGTGGCGAG 666

Qy      1538 GCAAGGTGAGATGCTGAGGGAGGACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAA 1597
          ||||| ||||| ||||| ||||| || |||| || || ||
Db      667 GCAAGGTGAGACTCTGAGGAAGGACTGAGGAGGCCCCACCCAAGATAGA-GGAACCCAA 725

Qy      1598 ATGATCCAGTACCACCCCTGCTGCCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAG 1657
          || ||||| || ||||| ||||| ||||| || || |||||
Db      726 ATAATCCAGCCACGTCCTGCTGCCAGTCTGGACCACCCGG---GGGAAGACTTCTCA- 781

Qy      1658 CTGGACCACCCCCGTCCTGCTCCCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATA 1717
          || || || || ||||| ||||| || || ||||| || |||||
Db      782 ---GGCTAGGCCATCCCAGTCCCCTGCTGCCACTAAAGCTACAGGGGACTCTAGAGTCA-- 836

Qy      1718 GCTTATGTGACCGGGGCAGGGTTGGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGC 1777
          |||| || || |||||
Db      837 -----AGAGCTTGGTGTGCCCAAGGCAGGGCCAGG 866

Qy      1778 ATCCGCCCCGGCATTAGGGTCAGGACCCCTGGGAGGGAAGTGGGGTCCCCACCCACACCT 1837
          || || || ||||| ||||| || ||||| ||||| || ||||| |||||
Db      867 CTCTGCCTGGCATCGGGTCAGGACCTTGAGAGGGAAGTGGGGCGCTACACCCCAACC 926

Qy      1838 GTCTCCTCATCTCCACCGCCACCCCACTCACATTCCCATACCTACCCCTACCCCAACC 1897
          || || || || ||||| || || || || ||
Db      927 CATCCGCATTC-----CAACATGCCAGCCCCATCCCCAAGTCCGTTTTCAGAA 976

Qy      1898 TCATCTTGTGAGAATCCCTGCTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCAC 1957
          || || || ||||| ||||| ||||| || ||||| |||||
Db      977 TCCATTTTT---TCCCCTGCAAGTCAACCCCGGAAGACCTGGGAATGGT---CAGGCAC 1029

Qy      1958 TCGGATCTTGACGTCCCCATCCAGGGTCTGATGGAGGGAAGGG-----GCTTGAACAG 2010
          ||||| ||||| ||||| || || || || || || || || || ||
Db      1030 TCGGATCTTGACATCCACATCGAGGGCTGAAGGAGGAGAGAGTTTGGTATCATGAGCAG 1089

Qy      2011 GGCCTCAGGGGAGCAGAGGGAG-----GGCCCTACTGCGAGATGAGGGAGGCCTCAGAG 2064
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Db      1090 AGCCTCAGGGTAGCAGAGGGAGGACCCCTGGCCCTCTGGGAGATGAGGAAGGCCTCAGGA 1149

Qy      2065 GACCCAGCACCC-----TAGGACACCGCACCCCTGTCTGAGACTGAG--GCTGCCA 2113
          ||||| ||||| || ||||| ||||| ||||| ||||| || ||
Db      1150 GACCCAGCACCCCAAGGCAGGGAGCCACCCACCCCTGTCTGAGAATGAGGTGCCTCCT 1209

Qy      2114 CTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGGGTGGGA--CCCAG 2171
          || || ||||| ||||| || ||||| ||||| || || || || || ||
Db      1210 CCTTTAGCCTCAGGAATCCAAGGGATGGCAACTCAGGTCAGCAGAGGGGTGGGTCCAAG 1269

Qy      2172 GCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTTGGAAATCCAGAT 2231
          ||| || || || || ||||| ||||| ||||| ||||| ||||| |||||
Db      1270 CCCTTCCAGGATCAAGGAAAGGAAGACGAGGGAGGATTAGGGGGCCTTGCAATCCAGAT 1329

Qy      2232 CAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATGGCCCATATTTTC 2291
          |||| ||||| ||||| ||||| ||||| ||||| || || ||||| || ||
Db      1330 CAGTGGAGACCTGGGCCCTGGGAGGTCTGGGCAAGGTAGCCACCTGTAGCTCATACTTC 1389

Qy      2292 CTGCATCTTTGAGGT----GACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTC 2347

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Db	1390	CTGCATCTTCGAGGTCACAGAGAGGAGAGGGCTATGGTCTGAGGGGTGGTACTTCAGGTC	1449
Qy	2348	AACAGAGGGAGGAGTTCCAGGATCCATATGGCCCCAAGATGTGCC-CCCTTCATGAGGACT	2406
Db	1450	CGCAGAGGGAGGAGTCCCAGGATCTACAGGACCCAAGGTGTGCCACACTTCACGAGGAAT	1509
Qy	2407	GGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTTTTAGTA	2466
Db	1510	GGGGATACCTGTGGCTCAGAAAGACGGGACCCACAGAGTCTGGCTGTCCCCGTGTTCTTA	1569
Qy	2467	GCTCTAGGGGGACAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCACAGGCA	2526
Db	1570	GCTCAGGGGGACAGAGGAGGGATGGCCCTATGTGCCAATTTCACTTGTTCACAGGCA	1629
Qy	2527	GGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCTACTCAT	2586
Db	1630	GGAAGTTGGGGAACCTTCAGGGAGATGAGGTTTGGAGTAAAGGGGCAATGTTGCTCAT	1689
Qy	2587	GTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGTGAGACA	2646
Db	1690	CTCAGGGGGTTGGGGGTTGAGGAAGGCAGGCCCTGTCAGGAGCAAACATGAGT-ACCCA	1748
Qy	2647	GACAAGGCTATTGGAATCCACACCCAGAACCAAAGGGGTAGCCCTGGACACCTCACCC	2706
Db	1749	CAGGAGGCCATCAGAACCCTCACCCAGAACCAAAGGGGTAGCCCTGGGCACCCACAC	1808
Qy	2707	AG-----GATGTGGCTTCTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGAC	2758
Db	1809	AGGGGTGACAGGATGTGGCTCCTTCTCATTTCTGATTCCAGATCTCAGTGAGGTGAGGAC	1868
Qy	2759	CTCATTTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAG	2818
Db	1869	CTTGTTCTCAGAGGGTGACTCAGGTACACAGGGACCCCCATCTGGTCTACAGACACAG	1928
Qy	2819	CGGTCCCAGGATCTGCCATGCGTTCTGGGTGAGGAACATGAGGGAGGACTGAGGGTACCC	2878
Db	1929	TGGTCCCAGGATCTGCCAAGAGTCTGGTGAGGAATGTGAGGGAGGATTGAGGGTACCAC	1988
Qy	2879	AGGACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGTCTGCACCCAG	2938
Db	1989	AGGGCCAGAACGCAGATGATGACCCACAGAAATCAGCCCTGTCTCTGTTGTACCCAG	2048
Qy	2939	AGAGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCTGGGATCATTGATGTCAG	2998
Db	2049	AGAGCATGGGCTTGGCTTTCTGCTGAGGTCCCTCTCTTATCTGAGGATCACTGGTGTAC	2108
Qy	2999	GGACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGG	3058
Db	2109	GGAGGGGGAGGCCTTGGTCTGAGGGGGCTGCACCCAGGTCAGTAGAGGGAGGGTCCCAGG	2168
Qy	3059	CCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCA	3118
Db	2169	CTCTGCCAGGAGTTGAGGTGAGGACCAAGCAGGCTCCGCATCCAGGACACATGGGTCCA	2228
Qy	3119	ATGAATTTTGATATCTCTTGCTGCCCTTC-CCCAAGGACCTAGGCACGTGTGGCCAGATG	3177
Db	2229	ATGAATTTGCACATCTTTTGCTGTCGTTCTTCGGAAGACCTAGGCACAGGTGGCCAGATG	2288
Qy	3178	TTTGTCCCCTCCTGTCCCTTCATTTCCTTATCATGGATGTGAACCTTTGATTGGATTCT	3237

Db	2289	TGGGGTTTCTTAGGTCTCT---GTTCCCTCTCAGGCATGTGAGCTCTTGATCTGAGTTTCT	2345
Qy	3238	CAGACCAGCAAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGA	3297
Db	2346		
Qy	3298	CAGGCCAGCAAAAAGAGTGGGATCCAGGCCCTGCCTGGAGAAATGTGAGGGCCCTGAGTGA	2405
Db	2406	GAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCCTC	3357
Qy	3358		
Db	2406	ACACAGTGGGGATCATCCACTCCATGAGAGTGGGGACCTCACAGAGTCCAGCCTACCCTC	2465
Qy	3417	CTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATT	3417
Db	2466		
Qy	3418	TTGATGGCACTGAGGGACCGGGCTGTGCTTACAGTCTGCACCCTAAGGGCCCATGGATT	2525
Db	2526	CCTCTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAG	3477
Qy	3478		
Db	2586	CCTCTCCTAGGAGCTCCAGGAACAAGGCAGTGAGGCCTTGGTCTGAGACAGTGTCTCCTCAG	2585
Qy	3537	GTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACAC	3537
Db	2586		
Qy	3538	GTTACAGAGCAGAGGATGCACAGGCTGTGCCAGCAGTGAATGTTGCCCTGAATGCACAC	2645
Db	2646	CAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTA	3597
Qy	3598		
Db	2706	CAAGGGCCCCACCTGCCACAAGACACATAGGACTCCAAAGAGTCTGGCCTCACCTCCCTA	2705
Qy	3657	CTGTCAGTCCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGA-GTACCCTCTCACT	3656
Db	2706		
Qy	3657	CCATCAATCCTGCAGAATCGACCTCTGCTGGCCGGCTATAACCTGAGGTGCTCTCTCACT	2765
Db	2766	TCCTCCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCAC	3716
Qy	3717		
Db	2825	TCCTCCTTCAGGTTCTGAGCAGACAGGCCAA-CCGGAGGACAGGATTCCCTGGAGGCCAC	2824
Qy	3777	AGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACT	3776
Db	2885		
Qy	3777	AGAGGAGCACCAAGGAGAAGATCTGTAAGTAAGCCTTTGTTAGAGCCTTAAGATTTGGT	2884
Db	2885	TCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCC	3836
Qy	3837		
Db	2945	TCTCAGCTGAGGTCTCTCATATGCTCCCTCTCTCCGTAGGCCTGTGGGTCCCCATTGCC	2944
Qy	3837	AGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGA	3896
Db	2945		
Qy	3897	AGCTTTTGCTGCACTCTTGCTGCTGCCCTGAGCAGAGTCATCATGTCTCTTGAGCAGA	3004
Db	3005	GGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG	3956
Qy	3957		
Db	3065	AGAGTCAGCACTGCAAGCCTGAGGAAGGCGTTGAGGCCCAAGAAGAGGCCCTGGGCCTGG	3064
Qy	3957	TGTGTGTGCAGGCTGCCAC-----CTCCTCCTCCTCTCCTC	3992
Db	3065		
Qy	3993	TGGGTGCGCAGGCTCCTACTACTGAGGAGCAGGAGGCTGCTGTCTCCTCCTCCTCCTC	3124
Db	3125	TGGTCTTGGGCACCTTGGAGGAGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTC	4052
Qy	4053		
Db	3185	TGGTCCCTGGCACCCTGGAGGAAGTGCTGCTGCTGAGTCAGCAGGTCTCCTCCCCAGAGTC	3184
Qy	4112	CTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTG	4112
Db	3185		
Qy	4112	CTCAGGGAGCCTCTGCCTTACCCACTACCATCAGCTTCACTTGTCTGGAGGCAACCCAATG	3244
Db	3244		



[illegible]



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; SEQ ID NO 147
;   LENGTH: 4895
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-482-029-147
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Query Match          44.3%;   Score 2513.6;   DB 9;   Length 4895;
Best Local Similarity 79.9%;   Pred. No. 0;
Matches 3415;   Conservative    0;   Mismatches 694;   Indels 165;   Gaps 32;
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Qy      1478 ATGGTTCTGAGGGGCGGCTTGAGATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAG 1537
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Db      607 ATAGTCCTGAGGGGCCAGTTGAGATCGGCTGAGGGGAGCGGGCCCAAGCTCTGTGGCGAG 666

Qy      1538 GCAAGGTGAGATGCTGAGGGAGGACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAA 1597
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      667 GCAAGGTGAGACTCTGAGGAAGGACTGAGGAGGCCCCACCCAAGATAGA-GGAACCCAA 725

Qy      1598 ATGATCCAGTACCACCCCTGCTGCCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAG 1657
          || ||||| | ||||| ||||| ||||| || |||||
Db      726 ATAATCCAGCCCACGTCTGCTGCCAGTCTTGGACCACCCGG---GGGAAGACTTCTCA- 781

Qy      1658 CTGGACCACCCCCGTCCTGCTCCCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATA 1717
          || | || | ||||| ||||| || ||||| || |||||
Db      782 ---GGCTAGGCCATCCCAGCTCCCACTGCCACTAAAGCTACAGGGGACTCTAGAGTCA-- 836

Qy      1718 GCTTATGTGACCGGGCAGGGTTGGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGC 1777
                               |||| || | |||||
Db      837 -----AGAGCTTGGTGTGCCCAAGGCAGGGCCAGG 866

Qy      1778 ATCCGCCCAGCATTAGGGTCAGGACCCCTGGGAGGGAAGTGGGGTCCCCACCCACACCT 1837
          || || ||||| ||||| ||||| ||||| || |||||
Db      867 CTCTGCCTGGCATCGGGTCAGGACCTTGAGAGGGAAGTGGGGCGCTACACCCCCACCC 926

Qy      1838 GTCTCCTCATCTCCACCGCCACCCCACTCACATTCCCATACCTACCCCTACCCCCAACCC 1897
          | || | || || ||||| || |||||
Db      927 CATCCGCATTC-----CAACATGCCAGCCCCATCCCCAATCCGTTTTCAGAA 976

Qy      1898 TCATCTTGTCAGAATCCCTGCTGTCAACCCACGGAAGCCACGGAATGGCGGCCAGGCAC 1957
          || || | ||||| ||||| ||||| || ||||| |||||
Db      977 TCCATTTTT---TCCCTGCAGTCAACCCCGGAAGACCTGGGAATGGT---CAGGCAC 1029

Qy      1958 TCGGATCTTGACGTCCCATCCAGGGTCTGATGGAGGGAAGGG-----GCTTGAACAG 2010
          ||||| ||||| ||||| || || || || |||||
Db      1030 TCGGATCTTGACATCCACATCGAGGGCTGAAGGAGGAGAGAGTTTGGTATCATGAGCAG 1089

Qy      2011 GGCCTCAGGGGAGCAGAGGGAG-----GGCCCTACTGCGAGATGAGGGAGGCCTCAGAG 2064
          ||||| ||||| ||||| ||||| ||||| |||||
Db      1090 AGCCTCAGGGTAGCAGAGGGAGGACCCCTGGCCCTCTGGGAGATGAGGAAGGCCTCAGGA 1149

Qy      2065 GACCCAGCACCC-----TAGGACACCGCACCCCTGTCTGAGACTGAG--GCTGCCA 2113
          ||||| || ||||| ||||| ||||| ||||| |||||
Db      1150 GACCCAGCACCCAAGGCAGGGAGCCACCCACCCCTGTCTGAGAATGAGGTGCCTCCT 1209

Qy      2114 CTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGGGTGGGA--CCCAG 2171
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Db      1210 CCTTTAGCCTCAGGAATCCAAGGGATGGCAACTCAGGTCAGCAGAGGGGTGGGTTCAG 1269

Qy      2172 GCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTTGGAAATCCAGAT 2231
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Db      1270 CCCTTCCAGGATCAAGGAAAGGAAGACGAGGGAGGATTGAGGGGCTTGCATTCCAGAT 1329
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Qy	2232	CAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATGCCCCATATTTTC	2291
Db	1330	CAGTGGAGACCTGGGCCCTGGGAGGTCTGGGCAAGGTAGCCACCTGTAGCTCATACTTC	1389
Qy	2292	CTGCATCTTTGAGGT----GACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTC	2347
Db	1390	CTGCATCTTCGAGGTCACAGAGAGGAGAGGGCTATGGTCTGAGGGGTGGTACTTCAGGTC	1449
Qy	2348	AACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCC-CCCTTCATGAGGACT	2406
Db	1450	CGCAGAGGGAGGAGTCCCAGGATCTACAGGACCAAGGTGTGCCACACTTCACGAGGAAT	1509
Qy	2407	GGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCTTTTAGTA	2466
Db	1510	GGGGATACCTGTGGCTCAGAAAGACGGGACCCACAGAGTCTGGCTGTCCCTGTTCTTA	1569
Qy	2467	GCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCACAGGCA	2526
Db	1570	GCTCAGGGGGACCAGAGGAGGGATGGCCCTATGTGCCAATTCACTTGTTCACAGGCA	1629
Qy	2527	GGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGATGTCTACTCAT	2586
Db	1630	GGAAGTTGGGGAACCTTCAGGGAGATGAGGTTTTGGAGTAAAGGGGCAATGTTTGCTCAT	1689
Qy	2587	GTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGTGAGACA	2646
Db	1690	CTCAGGGGGTTGGGGTTGAGGAAGGGCAGGCCCTGTCAGGAGCAAACATGAGT-ACCCA	1748
Qy	2647	GACAAGGCTATTGGAATCCACACCCAGAACCAAGGGGTCAGCCCTGGACACCTCACCC	2706
Db	1749	CAGGAGGCCATCAGAACCTCACCCAGAACCAAGGGGTCAGCCCTGGGCACCCACAC	1808
Qy	2707	AG-----GATGTGGCTTCTTTTTCCTCTGTTTCCAGATCTGGGGCAGGTGAGGAC	2758
Db	1809	AGGGGTGACAGGATGTGGCTCCTTCTCATTTCTGATTCCAGATCTCAGTGAGGTGAGGAC	1868
Qy	2759	CTCATTCTCAGAGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAG	2818
Db	1869	CTTGTTCTCAGAGGTGACTCAGGTCAACACAGGGACCCCATCTGGTCTACAGACACAG	1928
Qy	2819	CGGTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCC	2878
Db	1929	TGGTCCCAGGATCTGCCAAGAGTCTTGGTGAGGAATGTGAGGGAGGATTGAGGGTACCAC	1988
Qy	2879	AGGACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGTCTGTACCCACAG	2938
Db	1989	AGGGCCAGAACGCAGATGATGACCCACAGAAATCAGCCCTGTCTCTGTGTGTACCCACAG	2048
Qy	2939	AGAGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAG	2998
Db	2049	AGAGCATGGGCTTGGCTTCTGTCTGAGGTCCCTCTCTTATCCTGGGATCACTGGTGTAC	2108
Qy	2999	GGACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGG	3058
Db	2109	GGAGGGGGAGGCCCTTGGTCTGAGGGGGCTGCACCCAGGTCAGTAGAGGGAGGGTCCCAGG	2168
Qy	3059	CCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCA	3118
Db	2169	CTCTGCCAGGAGTTGAGGTGAGGACCAAGCAGGCTCCGCATCCAGGACACATGGGTTCCA	2228

Qy 3119 ATGAATTTTGATATCTCTTGCTGCCCTTC-CCCAAGGACCTAGGCACGTGTGGCCAGATG 3177  
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 Db 2229 ATGAATTTTCGACATCTTTTGCTGTCGTTCTTCGGAAGACCTAGGCACAGGTGGCCAGATG 2288

Qy 3178 TTTGTCCCCCTCCTGTCTTCCATTCCATTATCATGGATGTGAACCTTTGATTGGATTCT 3237  
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 Db 2289 TGGGGTTTCTTAGGTCCT---GTTCCCTCTCAGGCATGTGAGCTCTTGATCTGAGTTTCT 2345

Qy 3238 CAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGA 3297  
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 Db 2346 CAGGCCAGCAAAAGAGTGGGATCCAGGCCCTGCCAGGAAAATGTGAGGGCCCTGAGTGA 2405

Qy 3298 GAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCACCCCTC 3357  
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 Db 2406 ACACAGTGGGGATCATCCACTCCATGAGAGTGGGGACCTCACAGAGTCCAGCCTACCCTC 2465

Qy 3358 CTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCTGAGGGCCCGTGGATT 3417  
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 Db 2466 TTGATGGCACTGAGGGACCGGGCTGTGCTTACAGTCTGCACCTAAGGGCCCATGGATT 2525

Qy 3418 CCTCTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAG 3477  
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 Db 2526 CCTCTCCTAGGAGCTCCAGGAACAAGGCAGTGAGGCCTTGGTCTGAGACAGTGTCTCAG 2585

Qy 3478 GTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACAC 3537  
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 Db 2586 GTTACAGAGCAGAGGATGCACAGGCTGTGCCAGCAGTGAATGTTGCCCTGAATGCACAC 2645

Qy 3538 CAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTA 3597  
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 Db 2646 CAAGGGCCCCACCTGCCACAAGACACATAGGACTCCAAAGAGTCTGGCCTCACCTCCCTA 2705

Qy 3598 CTGTCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGA-GTACCCTCTCACT 3656  
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 Db 2706 CCATCAATCCTGCAGAATCGACCTCTGCTGGCCGGCTATACCCTGAGGTGCTCTCTCACT 2765

Qy 3657 TCCTCCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCAC 3716  
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 Db 2766 TCCTCCTTCAGGTTCTGAGCAGACAGGCCAA-CCGGAGGACAGGATTCCCTGGAGGCCAC 2824

Qy 3717 AGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACT 3776  
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 Db 2825 AGAGGAGCACCAAGGAGAAGATCTGTAAGTAAGCCTTTGTTAGAGCCTTAAGATTTGGT 2884

Qy 3777 TCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCC 3836  
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 Db 2885 TCTCAGCTGAGGTCTCTCACATGCTCCCTCTCTCCGTAGGCCTGTGGGTCCCCATTGCC 2944

Qy 3837 AGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGATCATCATGTCTCTTGAGCAGA 3896  
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 Db 2945 AGCTTTTGCCCTGCACTCTTGCTGCTGCCCTGAGCAGAGTCATCATGTCTCTTGAGCAGA 3004

Qy 3897 GGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG 3956  
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 Db 3005 AGAGTCAGCACTGCAAGCCTGAGGAAGGCGTTGAGGCCCAAGAAGAGGCCCTGGGCCTGG 3064

Qy 3957 TGTGTGTGCAGGCTGCCAC-----CTCCTCCTCCTCTCCTC 3992  
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 Db 3065 TGGGTGCGCAGGCTCCTACTACTGAGGAGCAGGAGGCTGCTGTCTCCTCCTCCTCCTC 3124

Qy 3993 TGGTCCTGGGCACCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCTCCCCAGAGTC 4052

Db	3125		
		TGGTCCCTGGCACCCCTGGAGGAAGTGCCTGCTGCTGAGTCAGCAGGTCCTCCCCAGAGTC	3184
Qy	4053	CTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTG	4112
Db	3185	CTCAGGGAGCCTCTGCCTTACCCACTACCATCAGCTTCACTTGCTGGAGGCAACCCAATG	3244
Qy	4113	AGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGT	4172
Db	3245	AGGGTTCCAGCAGCCAAGAAGAGGAGGGGCCAAGCACCTCGCCTGACGCAGAGTCCTTGT	3304
Qy	4173	TCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATC	4232
Db	3305	TCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGCTCATTTTCTGCTCCGCAAGTATC	3364
Qy	4233	GAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGC	4292
Db	3365	GAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGAGAGTCATCAAAAATTACAAGC	3424
Qy	4293	ACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTG	4352
Db	3425	GCTGCTTTCTGTGATCTTCGGCAAAGCCTCCGAGTCCCTGAAGATGATCTTTGGCATTG	3484
Qy	4353	ACGTGAAGGAAGCAGACCCACCGGCCACTCTATGTCCTTGTACCTGCCTAGGTCTCT	4412
Db	3485	ACGTGAAGGAAGTGGACCCACCAAGCAACACCTACACCCTTGTACCTGCCTGGGCCTTT	3544
Qy	4413	CCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTG	4472
Db	3545	CCTATGATGGCCTGCTGGGTAAATAATCAGATCTTTCCCAAGACAGGCCCTCTGATAATCG	3604
Qy	4473	TCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGC	4532
Db	3605	TCCTGGGCACAATTGCAATGGAGGGCGACAGCGCCTCTGAGGAGGAAATCTGGGAGGAGC	3664
Qy	4533	TGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGC	4592
Db	3665	TGGGTGTGATGGGGTGTATGATGGGAGGGAGCACACTGTCTATGGGGAGCCCAGGAAC	3724
Qy	4593	TGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTG	4651
Db	3725	TGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTACCCGGCAGTA	3784
Qy	4652	ATCCCGCACGCATGAGTTCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGA	4711
Db	3785	ATCCTGCGCGCTATGAGTTCTGTGGGGTCCAAGGGCTCTGGCTGAAACCAGCTATGTGA	3844
Qy	4712	AAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGC	4771
Db	3845	AAGTCCTGGAGCATGTGGTCAGGGTCAATGCAAGAGTTCGCATTGCCTACCCATCCCTGC	3904
Qy	4772	GTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCA	4831
Db	3905	GTGAAGCAGCTTTGTTAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAGGGCTG	3964
Qy	4832	GTGGGAGGG----GGAAGTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCTT	4887
Db	3965	TGGGGAAGGGGCAGGGCTGGGCCAGTGCATCTAACA--GCCCTGTGCAGCAGCTTCCCTT	4022
Qy	4888	GCCTCGTGTGACATGAGGCCATTCTTCACTC----TGAAGAGAGCGGTGAGTGTCTCA	4943

Db 4023 GCCTCGTGTAAACATGAGGCCCATCTTCACTCTGTTTGAAGAAAATAGTCAGTGTCTTA 4082

Qy 4944 GTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCTTTTGGGAATT 5003  
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Db 4083 GTAGTGGGTTTCTATTTTGTGGATGACTTGGAGATTATCTCTGTTTCCTTTTACAATT 4142

Qy 5004 GTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGTTTATGAATG 5063  
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Db 4143 GTTGAAATG-TTCCTTTTAATGGATGGTTGAATTAACCTCAGCATCCAAGTTTATGAATC 4201

Qy 5064 ACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAG 5123  
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Db 4202 GTAGTTAACGTATATTGCTGTTAATATAGTTTAGGAGTAAGAGTCTTGTTTTTATTTCAG 4261

Qy 5124 ATTGGGAAATCCATTCTATTTTGTGAATTGGG---ATAATAACAGCAGTGGAAATAAGTAC 5180  
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Db 4262 ATTGGGAAATCCGTTCTATTTTGTGAATTTGGGACATAATAACAGCAGTGGAGTAAGTAT 4321

Qy 5181 TTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAATTAAGAG 5240  
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Db 4322 TTAGAAGTGTG---AATTCACCGTGAAATAGGTGAGAT-----AAATTAAG 4366

Qy 5241 ATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATATGCAT 5300  
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Db 4367 ATACTTAATTCGCGCTTATGCCTCAGTCTATTCTGTAAAATTTAAAAATATATATGCAT 4426

Qy 5301 ACCTGGATTTCCCTTGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAGAATTC 5360  
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Db 4427 ACCTGGATTTCCCTTGCTTC---GTGAATGTAAGAGAAATTAAATCTGAATAAATAATTC 4483

Qy 5361 TTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAAGGCCCT 5420  
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Db 4484 TTTCTGTTAACTGGCTCATTTCTTCTCTATGCACTGAGCATCTGCTCTGTGGAAGGCCCA 4543

Qy 5421 GGGTTAGTAGTGGAGATGCTAAGGTAAAGCCAGACTCATACCCACCCATAGGGTCGTAGAG 5480  
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Db 4544 GGATTAGTAGTGGAGATACTAGGGTAAGCCAGACACACCTACCGATAGGGTATTAAGA 4603

Qy 5481 TCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAGGGAAAA 5540  
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Db 4604 GTCTAGGAGCGCGGTCATATAATTAAGGTGACAAGATGTCTCTAAGATGTAGGGAAAA 4663

Qy 5541 GTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGCCCTGA 5600  
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Db 4664 GT---AACGAGTGTGGGTATGGGGCTCCAGGTGAGAGTGGTCGGGTGTAAATTCCCTGT 4719

Qy 5601 GCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCTTCTGGGGGAGCTGATTGTAATGA 5660  
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Db 4720 G-TGGGGCCTTTTGGGCTTTGGGAAACTCCATTTTCTTCTGAGGGATCTGATTCTAATGA 4778

Qy 5661 TCTTGGGTGGATCC 5674  
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Db 4779 AGCTTGGTGGGTCC 4792

RESULT 4  
 US-10-482-029-87  
 ; Sequence 87, Application US/10482029  
 ; Publication No. US20050037445A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ODIN medical A/S

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; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 4741
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-482-029-87

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Query Match          42.7%; Score 2422.8; DB 9; Length 4741;
Best Local Similarity 75.7%; Pred. No. 0;
Matches 3726; Conservative 0; Mismatches 882; Indels 314; Gaps 46;

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QY      715 TTCCCGCCAGGAAACATCCGGGTGCCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGG 774
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Db      15 TTCAACCCAGGGAATCCCTGGGTGACCAGATGTGGTGCCACTGTCTTGCACATTTGAGGT 74

QY      775 CAGAGAGAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGA 834
      | ||||| ||| | || |||| | || || || || || || || ||
Db      75 CGGAGAGAAGCAAGGGCTCGCTCTCAGGGGCAGC-TGGAGATCAGCTGAGGGCAGCTGG 133

QY      835 CCCAGGCTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTC 894
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||| ||
Db      134 CCCTGGCTCTGTGAGGATGCAAGGTGAGATGCTGAGGGAGGACTAAGGAGTATCCCACCC 193

QY      895 CAAATAGAGAGCCCCAAATATTCCAG---CCCCGCCCTTGCTGCCAGCCCTGGCCCCACCC 951
      | ||| | ||||| ||||| | || | ||||| ||| |||| ||| ||
Db      194 CTGGTAGTGAGACCCCAAATAATCCAGTGCCACCTCTCCTGCTGCTAGCTCTGGACCATCC 253

QY      952 GCGGGAAGACGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGAC 1011
      || | ||| || || ||||| ||||| |||| | || |||| | |||
Db      254 AGGGCAGGACTTCTTAGGCTGGGCCACCCCCAGTCCCCCACCGCTTAAGCCGCAGGGGA- 312

QY      1012 ACCAGGTTCTTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGT 1071
      ||| ||| ||||| ||| | ||||| ||||| ||||| ||||| |||||
Db      313 -----CTCAGGAGACAGAGCTTGGTATGACCAGGGCAGGACTGGT 352

QY      1072 TAGGAGAGGGCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGC 1131
      ||||| ||| | || ||||| ||||| | ||| |||| | || | ||| |
Db      353 TAGGAGAGGACAGTCCCA-GCTCTGCCAGGAAACAACGTCAGGAACCTAAGGGAAAGCT 411

QY      1132 TGTGGGCCCCCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCC 1191
      | ||||
Db      412 GAGGCTACCCC----- 422

QY      1192 CACCCAACCCCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCAC 1251
      |||| | | | | || ||| |||| | |||
Db      423 -----CACCCAAACTCTATTCTGTCCCTACCTCCGTCC 457

QY      1252 CTGACCACCACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCCTCACT 1311
      | ||| |||| ||| || || |||| |||| | ||||| || |||
Db      458 CCCACCTACACCCCCATTCC-----CCCACCCCTTCCCTACCGGCACCTCTATCCCACA 512

QY      1312 GCCCCCAACCCACCCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATTTCTG 1371
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Db      513 TCCCCCA-----CCCCATCCTG 530

QY      1372 GCAGAATCCGGTT-TGCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCGATGTGAA 1430

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Db	531	GCAGAATCCGATTCTGCCCCTGATTTCAACCCAGGGAAGCCCTAGGGGGCCGGATGTGAT	590
Qy	1431	ACCACTGACTTGAACCTCACAGATCTGAGAGAAGCCAGGTTTCATTTAATGGTTCTGAGGG	1490
Db	591	GCTGCTGACTTGTGCATTGGGGGTGAGAGAGAATCAAGG-----GCATGGTTCTGAGAA	644
Qy	1491	GCGGCTTGAGATCCACTGAGGGGAGTGGTTTATAGGCTCTGTGAGGAGGCAAGGTGAGATG	1550
Db	645	GCCGACTGAGATCAGCAGAGGGGAATGGGCCCGGGCTCTGTGAGGAGGCAAGGTGAGACC	704
Qy	1551	CT-GAGGGAGGACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTAC	1609
Db	705	CCCGAGGAAGGAATGAGGAAGCCCTCACCC--AGATAGAGAACCCCAAATAATCCAGTAC	762
Qy	1610	CACCCCTGCTGCCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCC	1669
Db	763	TACCTTTGCTGCCAGCCCTGGACCAC----CCAGGGCAGACTTCTCAGGCTGAACCTTCC	818
Qy	1670	CCGTCCCGTCCCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTT-ATGTGAC	1728
Db	819	C---CCCTCCCCACTGCCACTTAAGCCACAAGGGACTCTGGAGTCAGACCTTGGTGTGAC	875
Qy	1729	CGGGGCAGGGTTGGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGC	1788
Db	876	CAGGGAAGGGCCGGTCAGGAGAGG-----GCAGGGGCCAGGCTCTGTCTAGGC	922
Qy	1789	ATTAGGGTCAGGACCCTGGGAGGGAAGTGAAGGGTTCACCCACACCTGTCTCCTCATC	1848
Db	923	ATCAAAATCAGGACCCCTGAGAGAGAATTGAGGGCCCCACCCCAACCCCTATACCCATCC	982
Qy	1849	TCCACCGCCACCCCACTCACATTCCCATACCTACC----CCCTACCCCCAACCTCATCTT	1904
Db	983	CTAACCCCATACCCACTCTACTTGCATTCCAGCCCCATCCCCACACCTACCCCATCTT	1042
Qy	1905	GTCAGAA-----TCCCTGCTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGG	1954
Db	1043	GGCAGAATCTGTTTCTTTCCCTGCAGTCAACCCACAGAAGCCCCAGGAATGACAGACAGG	1102
Qy	1955	CACCTCGGATCTTGACGTCCCCTATCCAGGGTCTGATGGAGGGAAGGG-----GCTTGAA	2007
Db	1103	CACACCTATCTTGACGTCCACATCCAGGGCTGAAGGAGGGAAGGGCTTAGTATCATGAG	1162
Qy	2008	CAGGGCCTCAGGGGAGCAGAGG-----GAGGGCCCTACTGCGAGATGAGGGAGGCCTCAGA	2063
Db	1163	CAGGGCCTCAGGGGAGTCTCTGCTCCTCAAGCCCTGCTGGGAGTAAAGGGAGGCCTCAGG	1222
Qy	2064	GGACCCAGCACCCTAGGA-----CACCGCACCCCTGTCTGAGACTGAG--GCTGCC	2112
Db	1223	GAACCCAGGTCCCTCAGGATAGGGGTCCACTCCAACCTGTCTGAGACTGAGGCGCCTCC	1282
Qy	2113	ACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGGGTGGGACCCAGG	2172
Db	1283	TCTTTTCATCCTCGGGAATCACAGGGATGGAGACTCACGTGAGCAGAGGGTGGGGCCCAAC	1342
Qy	2173	CCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTTGGAAATCCAGATC	2232
Db	1343	CCTGCCAGGATCAAGGAGAGGAAGAAGAGGGAGGACTCAGGGTACCTTTGAGTCCAGAAC	1402
Qy	2233	AGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATGGCCCATATTTC	2292

Db 1403 AATGGGGACCTTTGCCCTGGGAGGTCCAGTGCACAGTGGCCACCTGTAGCCCATGCTTGC 1462

Qy 2293 TGCATCTTTGAGGTGAC----AGGACAGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTCA 2348  
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Db 1463 TGCACCTTCTGGGTGACAAAGAGGAGAGGGCTGTGGTCAGAGCAGTGGTGACTCAGGTCA 1522

Qy 2349 ACAGAGGGAGGAGTTCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATGAGGACTGG 2408  
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Db 1523 GCAGAGGGAGGAGTCCCAGCATCTGCAGGCCCAATGTGTGCCCCATTTCATGAAGATTGG 1582

Qy 2409 GGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTTTTAGTAGC 2468  
 ||||| || ||||| ||||| ||||| ||||| ||||| ||||| || |||

Db 1583 GGATA-CCTTGGCTCAGAAAGAAGGGACCCACAGAGTCTGGCTGTCCCCTGATTTTTCG 1641

Qy 2469 TCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCATTGTACCACAGGCAGG 2528  
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Db 1642 TCAGAGGGGGACCAATCAAGGATAGCCCTATGTGCCAACCTCATTTGTGCCACAGGAAAG 1701

Qy 2529 AAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCTACTCATGT 2588  
 ||||| | ||||| ||||| ||||| ||||| || ||||| ||||| |

Db 1702 AAGTTGAAGAGCCCTCAGGGTGATGGGGTCTTGTCAGTAAAGGGGAGCTATCTGCTCATCT 1761

Qy 2589 CAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGTGAGACAGA 2648  
 ||||| || ||||| ||||| ||||| | ||||| || ||||| || |||

Db 1762 CAGGGGGTTTCAGGTTGAGGAATGGCAGGCCCATCACGATGAAGAGTAACCCACAGG-- 1819

Qy 2649 CAAGGCTATTGGAATCCACACCCCAAGAAAGGGGTAGCCCTGGACACCTCA----- 2703  
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Db 1820 ---AGCCATAGAAACACTACCCCAAGAAAGGGGTATACCTGGACACCCCATGTGG 1876

Qy 2704 ----CCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACC 2759  
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Db 1877 GGGTGACAGGATGTAGC-TCCATCTCATTCCGTGTTTTCAGATCTCGGGGAGGTGAGGAAC 1935

Qy 2760 TCATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGC 2819  
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Db 1936 TTGTTCTCCGAGGATGACTCAGGTCAACACAGGGGCCCATCTGGTGGATAGACAGAGT 1995

Qy 2820 GGTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCCA 2879  
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Db 1996 GGTCCCAGGATCTGTCTAGTAGTTCCGGTGAGGAACATGAGGGACGATTGAGGGCACCTT 2055

Qy 2880 GGACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCCA 2939  
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Db 2056 GGGCCAGAACACAGATGAGGACCTCACGGAATCTGCCCTGCCCTGCTGTCTACTCCAGA 2115

Qy 2940 GAGCATGGGCTGGGCCGTCTGCCGAGGTCTTCC--GTTATCCTGGGATCATTGATGTCA 2997  
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Db 2116 GAGCATGGGCAGGGCTGTCTGTCTGCAGTCCCCCACTTACCCTGGGATCATTTGGTGTCA 2175

Qy 2998 GGGACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAG 3057  
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Db 2176 GGGATGGGGAGGTCTTTGTC-GAGGGGTCTGCACTCAGGTCAGTAGAGGGAGCGTCTTAG 2234

Qy 3058 GCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCC 3117  
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Db 2235 GCCCTGCCAGGAGACAAGGTAAAGAACGAAGCAGGTTCTCACCCAGGACACATGAATTCC 2294

Qy 3118 AATGAATTTTGATATCTTGTCTGCCCTTCCCCA-AGGACCTAGGCACGTGTGGCCAGAT 3176  
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Db 2295 AATGCATTTTCAGCATCTCTTCTGTCTTCCCCAAGAGGACCTGGGCACGTGTGGCCAGAT 2354

Qy	3177	GTTCGTCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTTGATTTGGATTTC	3236
Db	2355	GTGAGTCTCCTCATGTCCT---GTTCCCTATCAGGGATGTGAGCTCTTAATCTGAGTTTC	2411
Qy	3237	TCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTG	3296
Db	2412	TCAGGCCAGCAAAAGGGTGGGATCCAGGCCCTGCCAGGAGAAAGGTGAGGGCCCTGTGTG	2471
Qy	3297	AGAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCT	3356
Db	2472	AGCACAGAGGGGACCATTACCCCAAGAGGGTGGAGACCTCACAGATTCCAGCCTACCT	2531
Qy	3357	CCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCTGGAT	3416
Db	2532	CCTGTTAGCACTGGGGGCCCTGAGGCTGTGCTTGCACTCTGCACCCTGAGGGCCCATGCAT	2591
Qy	3417	TCCTCTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCA	3476
Db	2592	TCCTCTTCCAGGAGCTCCAGGAACAGACACTGAGGCCTTGGTCTGAGGCCGTGCCCTCA	2651
Qy	3477	GGTCACAGAGCAGAGGATGCACAGGGT---GTGCCAGCAGTGAATGTTTGCCCTGAATG	3532
Db	2652	GGTCACAGAGCAGAGGAGATGCAGACGCTAGTGCCAGCAGTGAACGTTTGCTTGAATG	2711
Qy	3533	CACACCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCA-CC	3591
Db	2712	CACACTAATGGCCCCCATCGCCCCAGAACATATGGGACTCCAGAGCACCTGGCCTCACCC	2771
Qy	3592	TCCCTACTGTCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTC	3651
Db	2772	TCTCTACTGTCAGTCCTGCAGAATCAGCCTCTGCTTGCTTGTGTACCCTGAGGTGCCCTC	2831
Qy	3652	TCACTTCCTCCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGAC-----A	3698
Db	2832	TCACTTTTTCTCCTTCAGGTTCTCAGGGGACAGGCTGACCAGGATCACCAGGAAGCTCCAGA	2891
Qy	3699	GGATTCCCTGGAGGCCACAGAGGAGCACC-AAGGAGAAGATCTGTAAGTAGGCCTTTGTT	3757
Db	2892	GGATCCCCAGGAGGCCCTAGAGGAGCACCAAGGAGAAGATCTGTAAGTAAGCCTTTGTT	2951
Qy	3758	AGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGC	3817
Db	2952	AGAGCCTCCAAGGTTTCAGTTTTTAGCTGAGGCTTCTTCACATGCTCCCTCTCTCCAGGC	3011
Qy	3818	CTGTGGGTCTTCATTGCCAGCTCCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTC	3877
Db	3012	CAGTGGGTCTCCATTGCCAGCTCCTGCCACACTCCTGCCTGTTGCGGTGACCAGAGTC	3071
Qy	3878	ATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAA	3937
Db	3072	GTCATGTCTCTTGAGCAGAAGAGTCAGCACTGCAAGCCTGAGGAAGGCCTTGACACCCAA	3131
Qy	3938	CAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC-----C	3976
Db	3132	GAAGAGGCCCTGGGCCTGGTGGGTGTGCAGGCTGCCACTACTGAGGAGCAGGAGGCTGTG	3191
Qy	3977	TCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACA	4036
Db	3192	TCCTCCTCCTCTCCTCTGGTCCCAGGCACCCTGGGGGAGGTGCTGCTGCTGGGTCAACA	3251

Qy	4037	GATCCTCCCCAGAGTCTCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGA	4096
Db	3252	GGTCTCTCAAGAGTCTCTCAGGGAGCCTCCGCCATCCCCACTGCCATCGATTTCACCTCTA	3311
Qy	4097	CAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGT	4156
Db	3312	TGGAGGCAATCCATTAAGGGCTCCAGCAACCAAGAAGAGGAGGGGCCAAGCACCTCCCCT	3371
Qy	4157	ATCCTGGAGTCTTGTTCAGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTTT	4216
Db	3372	GACCCAGAGTCTGTGTTCCGAGCAGCACTCAGTAAGAAGGTGGCTGACTTGATTCATTTT	3431
Qy	4217	CTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTC	4276
Db	3432	CTGCTCCTCAAGTATTAAGTCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGAGCGTC	3491
Qy	4277	ATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCG	4336
Db	3492	ATCAAAAATTACAAGCGCTGCTTTCTGAGATCTTCGGCAAAGCCTCCGAGTCCTTGCG	3551
Qy	4337	CTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCCACCGCCACTCCTATGTCCTTGTC	4396
Db	3552	CTGGTCTTTGGCATTGACGTGAAGGAAGCGGACCCCCACAGCAACACCTACACCCTTGTC	3611
Qy	4397	ACCTGCC TAGGTCTCTCCTATGATGGCTGCTGGGTG---ATAATCAGATCATGCCCAAG	4453
Db	3612	ACCTGCC TGGG---ACTCCTATGATGGCTGCTGGTTGATAATAATCAGATCATGCCCAAG	3669
Qy	4454	ACAGGCTTCCTGATAATTGTCTGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAG	4513
Db	3670	ACGGGCC TCCTGATAATCGTCTTGGGCATGATTGCAATGGAGGGCAAATGCGTCCCTGAG	3729
Qy	4514	GAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCC	4573
Db	3730	GAGAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGTATGTTGGGAGGGAGCACAGTGTC	3789
Qy	4574	TATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGGTGCAGGAAAAGTACCTGGAGTA-	4632
Db	3790	TGTGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGGTGCAGGAAAAGTACCTGGAGTAC	3849
Qy	4633	CGGCAGGTGCCCGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTC	4692
Db	3850	CGGCAGGTGCCCAGCAGTGATCCCATATGCTATGAGTTACTGTGGGGTCCAAGGGCACTC	3909
Qy	4693	GCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTTCG	4752
Db	3910	GCTGCT-----TGAAAGTACTGGAGCACGTGGTCAGGGTCAATGCAAGAGTTCTC	3959
Qy	4753	TTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCA	4812
Db	3960	ATTTCTTACCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCA	4019
Qy	4813	TGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGT	4872
Db	4020	TGAGCTGCAGCCAGGGCCACTGCGAGGGGGGCTGGGCCAGTGCACCTTCCAGGGCTCCGT	4079
Qy	4873	CCAGCAGCTTCCCCTGCC-TCGTGTGACATGAGGCCATTCTTCACTC--TGAAGAGAGC	4929
Db	4080	CCAGTAGTTTCCCCTGCCTTAATGTGACATGAGGCCATTCTTCTCTTTGAAGAGAGC	4139
Qy	4930	GGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGT	4989

Db	4140	AGTCAACATTCTTAGTAGTGGGTTTCTGTTCTATTGGATGACTTTGAGATTTGTCTTTGT	4199
Qy	4990	TCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATC	5049
Db	4200	TTCTTTTGGGAATTGTTCAAATG-TTTCTTTTAATGGGTGGTTGAATGAAC TTCAGCATT	4258
Qy	5050	CAAGTTTATGAATGACAGCAGTCACAC--AGTTCTGTGTATATAGTTTAAGGGTAAGAGT	5107
Db	4259	CAAATTTATGAATGACAGTAGTCACACATAGTGCTGTTTATATAGTTTAGGAGTAAGAGT	4318
Qy	5108	CTTGTGTTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGG--ATAATAACAG	5165
Db	4319	CTTGTTTTTTATTTCAGATTGGGAAATCCATTCCATTTTGTGAATTGGGACATAGTTACAG	4378
Qy	5166	CAGTGGAATAAGTACTTA-GAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAA	5224
Db	4379	CAGTGGAATAAGTATTCATTTAGAAATGTGAATGAGCAGTAAAAC TGATGACA-----	4431
Qy	5225	CTAAAGAAATTAAGAGATAGTCAATTCTTGCC TTATACCTCAGTCTATTCTGTAAATTT	5284
Db	4432	-TAAAGAAATTAAGAGATATTTAATTCTTGCTTATACTCAGTCTATTCGGTAAATTTTT	4490
Qy	5285	TTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAA	5344
Db	4491	TTTAAAAAATGTGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGACAAATTAAA	4550
Qy	5345	TCTGAATAAAGAATTCTTCCTGTTCAGTGGCTCTTTTCTTCTCCATGCACTGAGCATCTG	5404
Db	4551	TCTGAATAAATCATCTCCCTGTTCAGTGGCTCATTTATTCTCTATGCACTGAGCATTTG	4610
Qy	5405	CTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCAC	5464
Db	4611	CTCTGTGGAAGGCCCTGGGTTAATAGTGGAGATGCTAAGGTAAGCCAGACTCACCCCTAC	4670
Qy	5465	CCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCT	5524
Db	4671	CCACAGGGTAGTAAAGTCTAGGAGCAGCAGTCATATAATTAAGGTGGAGAGATGCCCTCT	4730
Qy	5525	AA 5526	
Db	4731	AA 4732	

RESULT 5

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; SEQ ID NO 81  
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; ORGANISM: Homo sapiens  
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Query Match 42.4%; Score 2408; DB 7; Length 2420;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
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Db      1   GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          |||
Db      61   ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 3435
          |||
Db      121  CAGGGCTGTGCTTGCGGTCTGCACCCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
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Db      181  GGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTTGGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          |||
Db      241  CACAGGGTGTGCCAGCAGTGAATGTTTGGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 3615
          |||
Db      301  CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 360

Qy      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 3675
          |||
Db      361  CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 420

Qy      3676 GGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 3735
          |||
Db      421  GGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 480

Qy      3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 3795
          |||
Db      481  GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 540

Qy      3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT 3855
          |||
Db      541  CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT 600

Qy      3856 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 3915
          |||
Db      601  GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 660

Qy      3916 TGAGGAAGCCCTTGAGGCCCCACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 3975
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Db 661 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 720

Qy 3976 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCTTGGAGGAGGTGCCCACTGCTGGGTCAAC 4035  
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Db 721 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCTTGGAGGAGGTGCCCACTGCTGGGTCAAC 780

Qy 4036 AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTACTACCATCAACTTCACTCG 4095  
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Db 781 AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTACTACCATCAACTTCACTCG 840

Qy 4096 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG 4155  
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Db 841 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG 900

Qy 4156 TATCCTGGAGTCCTTGTTCGAGCAGTAATCATAAGAAGGTGGCTGATTGGTTGGTTT 4215  
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Db 901 TATCCTGGAGTCCTTGTTCGAGCAGTAATCATAAGAAGGTGGCTGATTGGTTGGTTT 960

Qy 4216 TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT 4275  
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Db 961 TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT 1020

Qy 4276 CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA 4335  
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Db 1021 CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA 1080

Qy 4336 GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT 4395  
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Db 1081 GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT 1140

Qy 4396 CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC 4455  
 |||

Db 1141 CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC 1200

Qy 4456 AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA 4515  
 |||

Db 1201 AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA 1260

Qy 4516 GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA 4575  
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Db 1261 GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA 1320

Qy 4576 TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAAGTACCTGGAGTA-CG 4634  
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Db 1321 TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAAGTACCTGGAGTACCG 1380

Qy 4635 GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC 4694  
 |||

Db 1381 GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC 1440

Qy 4695 TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT 4754  
 |||

Db 1441 TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT 1500

Qy 4755 TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG 4814  
 |||

Db 1501 TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG 1560

Qy 4815 AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGACCTTCCAGGGCCGCGTCC 4874  
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Db 1561 AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGACCTTCCAGGGCCGCGTCC 1620

Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTTCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCT	1740
Qy	4995	TTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT	5054
Db	1741	TTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATT CAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	5174
Db	1861	TTTATT CAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	1920
Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	5294
Db	1981	TAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	2040
Qy	5295	ATGCATACCTGGATTTCCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	5354
Db	2041	ATGCATACCTGGATTTCCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	2100
Qy	5355	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCAC TGAGCATCTGCTTTTTGGAA	5414
Db	2101	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCAC TGAGCATCTGCTTTTTGGAA	2160
Qy	5415	GGCCCTGGGT TAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	5474
Db	2161	GGCCCTGGGT TAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	2220
Qy	5475	G TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	5534
Db	2221	G TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	2280
Qy	5535	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG	5594
Db	2281	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG	2340
Qy	5595	CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG	5654
Db	2341	CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG	2400
Qy	5655	TAATGATCTTGGGTGGATCC	5674
Db	2401	TAATGATCTTGGGTGGATCC	2420

RESULT 6

US-10-741-466-5

; Sequence 5, Application US/10741466



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; Publication No. US20040180058A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, M.
; APPLICANT: Shneider, A.
; TITLE OF INVENTION: Vaccine Compositions and Methods
; FILE REFERENCE: 25955-003
; CURRENT APPLICATION NUMBER: US/10/741,466
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: 60/435,500
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Influenza A virus
US-10-741-466-5

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Query Match          42.4%; Score 2408; DB 9; Length 2420;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
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Db       1 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTGGTAGCACTGAGAAGC 3375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTCCTGGAGCTCCA 3435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTCCTGGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 3615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 360

Qy      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 3675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 420

Qy      3676 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 3735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 480

Qy      3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 3795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 540

Qy      3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCCACACTCCT 3855
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCCACACTCCT 600

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Qy	3856	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	3915
Db	601	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	660
Qy	3916	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	3975
Db	661	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	720
Qy	3976	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	4035
Db	721	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	780
Qy	4036	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	4095
Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG	4634
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG	1380
Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	1500

Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814
Db	1501	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	1560
Qy	4815	AGTTGCAGCCAAGGCCAGTGGGAGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	4874
Db	1561	AGTTGCAGCCAAGGCCAGTGGGAGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	1620
Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT	1740
Qy	4995	TTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	5054
Db	1741	TTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	5174
Db	1861	TTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	1920
Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAATTTTTAAAGATAT	5294
Db	1981	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAATTTTTAAAGATAT	2040
Qy	5295	ATGCATACCTGGATTTCCCTTGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	5354
Db	2041	ATGCATACCTGGATTTCCCTTGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	2100
Qy	5355	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAA	5414
Db	2101	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAA	2160
Qy	5415	GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	5474
Db	2161	GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	2220
Qy	5475	GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	5534
Db	2221	GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	2280
Qy	5535	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCATG	5594
Db	2281	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCATG	2340
Qy	5595	CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG	5654
Db	2341	CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG	2400
Qy	5655	TAATGATCTTGGGTGGATCC	5674

Db 2401 TAATGATCTTGGGTGGATCC 2420

RESULT 7

US-10-657-022-81  
; Sequence 81, Application US/10657022  
; Publication No. US20040180354A1  
; GENERAL INFORMATION:  
; APPLICANT: Simard, John J. L.  
; APPLICANT: Diamond, David C.  
; APPLICANT: Liu, Liping  
; APPLICANT: Liu, Zheng  
; TITLE OF INVENTION: EPITOPE SEQUENCES  
; FILE REFERENCE: MANNK.032A  
; CURRENT APPLICATION NUMBER: US/10/657,022  
; CURRENT FILING DATE: 2003-09-04  
; PRIOR APPLICATION NUMBER: 60/409123  
; PRIOR FILING DATE: 2002-09-06  
; NUMBER OF SEQ ID NOS: 610  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 81  
; LENGTH: 2420  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-657-022-81

Query Match 42.4%; Score 2408; DB 9; Length 2420;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	3256	GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC	3315
Db	1	GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC	60
Qy	3316	ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC	3375
Db	61	ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC	120
Qy	3376	CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA	3435
Db	121	CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA	180
Qy	3436	GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG	3495
Db	181	GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG	240
Qy	3496	CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA	3555
Db	241	CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA	300
Qy	3556	CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT	3615
Db	301	CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT	360
Qy	3616	CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTCAG	3675
Db	361	CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTCAG	420
Qy	3676	GGGACAGGCCAACCCAGAGGACAGGATTCCTGGAGGCCACAGAGGAGCACCAAGGAGAA	3735

Db 421 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACC AAGGAGAA 480

QY 3736 GATCTGTAAGTAGGCCTTTGT TAGAGTCTCCAAGGTT CAGTTCTCAGCTGAGGCCTCTCA 3795  
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Db 481 GATCTGTAAGTAGGCCTTTGT TAGAGTCTCCAAGGTT CAGTTCTCAGCTGAGGCCTCTCA 540

QY 3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT 3855  
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Db 541 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT 600

QY 3856 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 3915  
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Db 601 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 660

QY 3916 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 3975  
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Db 661 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 720

QY 3976 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 4035  
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Db 721 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 780

QY 4036 AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG 4095  
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Db 781 AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG 840

QY 4096 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG 4155  
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Db 841 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG 900

QY 4156 TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT 4215  
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Db 901 TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT 960

QY 4216 TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT 4275  
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Db 961 TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT 1020

QY 4276 CATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA 4335  
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Db 1021 CATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA 1080

QY 4336 GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT 4395  
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Db 1081 GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT 1140

QY 4396 CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCCAAGAC 4455  
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Db 1141 CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCCAAGAC 1200

QY 4456 AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA 4515  
 |||

Db 1201 AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA 1260

QY 4516 GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA 4575  
 |||

Db 1261 GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA 1320

QY 4576 TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG 4634  
 |||

Db 1321 TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG 1380

Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	1500
Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814
Db	1501	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	1560
Qy	4815	AGTTGCAGCCAAGGCCAGTGGGAGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	4874
Db	1561	AGTTGCAGCCAAGGCCAGTGGGAGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	1620
Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGAGATTTATCTTTGTTCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGAGATTTATCTTTGTTCTCT	1740
Qy	4995	TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	5054
Db	1741	TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGAAT	5174
Db	1861	TTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGAAT	1920
Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAAATTTTAAAGATAT	5294
Db	1981	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAAATTTTAAAGATAT	2040
Qy	5295	ATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	5354
Db	2041	ATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	2100
Qy	5355	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCAC TGAGCATCTGCTTTTTGGAA	5414
Db	2101	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCAC TGAGCATCTGCTTTTTGGAA	2160
Qy	5415	GGCCCTGGGT TAGTAGTGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	5474
Db	2161	GGCCCTGGGT TAGTAGTGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	2220
Qy	5475	G TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	5534
Db	2221	G TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	2280

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Qy      5535 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG 5594
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Db      2281 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG 2340

Qy      5595 CCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 5654
          |||
Db      2341 CCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 2400

Qy      5655 TAATGATCTTGGGTGGATCC 5674
          |||
Db      2401 TAATGATCTTGGGTGGATCC 2420

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RESULT 8

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US-10-807-308-17
; Sequence 17, Application US/10807308
; Publication No. US20040241725A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Wenming
; APPLICANT: Dong, Gang
; TITLE OF INVENTION: LUNG CANCER DETECTION
; FILE REFERENCE: 114122-00153
; CURRENT APPLICATION NUMBER: US/10/807,308
; CURRENT FILING DATE: 2004-03-24
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-807-308-17

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Query Match          42.4%; Score 2408; DB 9; Length 2420;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTTCATCC 3315
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Db      1 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          |||
Db      61 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGATTCTCTTCCTGGAGCTCCA 3435
          |||
Db      121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGATTCTCTTCCTGGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          |||
Db      181 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTTGGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          |||
Db      241 CACAGGGTGTGCCAGCAGTGAATGTTTGGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 3615
          |||
Db      301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 360

Qy      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTCAG 3675

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Db	361	CGACCTCTGCTGGCCGGCTGTACCCCTGAGTACCCCTCTCACTTCCTTCCTTCAGGTTTTCAG	420
Qy	3676	GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA	3735
Db	421	GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA	480
Qy	3736	GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA	3795
Db	481	GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA	540
Qy	3796	CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT	3855
Db	541	CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT	600
Qy	3856	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	3915
Db	601	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	660
Qy	3916	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	3975
Db	661	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	720
Qy	3976	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	4035
Db	721	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	780
Qy	4036	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	4095
Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGTTGGTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGTTGGTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575



Db 1261 GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA 1320

Qy 4576 TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG 4634  
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Db 1321 TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG 1380

Qy 4635 GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC 4694  
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Db 1381 GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC 1440

Qy 4695 TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT 4754  
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Db 1441 TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT 1500

Qy 4755 TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG 4814  
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Db 1501 TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG 1560

Qy 4815 AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC 4874  
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Db 1561 AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC 1620

Qy 4875 AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACCTCTGAAGAGAGCGGTCA 4934  
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Db 1621 AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACCTCTGAAGAGAGCGGTCA 1680

Qy 4935 GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT 4994  
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Db 1681 GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT 1740

Qy 4995 TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT 5054  
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Db 1741 TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT 1800

Qy 5055 TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT 5114  
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Db 1801 TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT 1860

Qy 5115 TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT 5174  
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Db 1861 TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT 1920

Qy 5175 AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT 5234  
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Db 1921 AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT 1980

Qy 5235 TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT 5294  
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Db 1981 TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT 2040

Qy 5295 ATGCATACCTGGATTTCCCTTGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA 5354  
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Db 2041 ATGCATACCTGGATTTCCCTTGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA 2100

Qy 5355 GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACGTAGCATCTGCTTTTGGAA 5414  
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Db 2101 GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACGTAGCATCTGCTTTTGGAA 2160

Qy 5415 GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC 5474  
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Db 2161 GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC 2220

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Qy      5475 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG 5534
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Db      2221 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG 2280

Qy      5535 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTC AATG 5594
          |||
Db      2281 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTC AATG 2340

Qy      5595 CCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 5654
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Db      2341 CCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 2400

Qy      5655 TAATGATCTTGGGTGGATCC 5674
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Db      2401 TAATGATCTTGGGTGGATCC 2420

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RESULT 9

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US-10-866-484-5
; Sequence 5, Application US/10866484
; Publication No. US20050013826A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, M.
; APPLICANT: Shneider, A.
; TITLE OF INVENTION: Vaccine Compositions and Methods
; FILE REFERENCE: 25955-003CIP
; CURRENT APPLICATION NUMBER: US/10/866,484
; CURRENT FILING DATE: 2004-06-11
; PRIOR APPLICATION NUMBER: 60/435,500
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 10/741,466
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Influenza A virus
US-10-866-484-5

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Query Match          42.4%; Score 2408; DB 9; Length 2420;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
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Db      1 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          |||
Db      61 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 3435
          |||
Db      121 CAGGGCTGTGCTTGCGGTCTGCACCCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCCTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          |||
Db      181 GGAACCAGGCAGTGAGGCCCTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

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Qy	3496	CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA	3555
Db	241	CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA	300
Qy	3556	CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT	3615
Db	301	CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT	360
Qy	3616	CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG	3675
Db	361	CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG	420
Qy	3676	GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA	3735
Db	421	GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA	480
Qy	3736	GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCCTCAGCTGAGGCCTCTCA	3795
Db	481	GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCCTCAGCTGAGGCCTCTCA	540
Qy	3796	CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT	3855
Db	541	CACACTCCCTCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT	600
Qy	3856	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	3915
Db	601	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	660
Qy	3916	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	3975
Db	661	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	720
Qy	3976	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	4035
Db	721	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	780
Qy	4036	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	4095
Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455

Db	1141		CACCTGCCTAGGTCTCTCCATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456		AGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGCCATGCTCCTGAGGA	4515
Db	1201		AGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGCCATGCTCCTGAGGA	1260
Qy	4516		GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261		GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576		TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG	4634
Db	1321		TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG	1380
Qy	4635		GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381		GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695		TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	4754
Db	1441		TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	1500
Qy	4755		TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814
Db	1501		TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	1560
Qy	4815		AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	4874
Db	1561		AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	1620
Qy	4875		AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621		AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935		GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCT	4994
Db	1681		GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCT	1740
Qy	4995		TTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	5054
Db	1741		TTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	1800
Qy	5055		TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801		TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115		TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	5174
Db	1861		TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	1920
Qy	5175		AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921		AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235		TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAAATTTTAAAGATAT	5294
Db	1981		TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAAATTTTAAAGATAT	2040
Qy	5295		ATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	5354

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Db      2041 ATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA 2100

Qy      5355 GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAA 5414
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Db      2101 GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAA 2160

Qy      5415 GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC 5474
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Db      2161 GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC 2220

Qy      5475 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG 5534
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG 2280

Qy      5535 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG 5594
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG 2340

Qy      5595 CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 5654
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 2400

Qy      5655 TAATGATCTTGGGTGGATCC 5674
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Db      2401 TAATGATCTTGGGTGGATCC 2420

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RESULT 10

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US-10-482-029-91
; Sequence 91, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-482-029-91

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Query Match          42.4%;  Score 2408;  DB 9;  Length 2420;
Best Local Similarity 99.9%;  Pred. No. 0;
Matches 2419;  Conservative 0;  Mismatches 0;  Indels 1;  Gaps 1;

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Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
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Db      1    GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61   ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTTCTTCTGGAGCTCCA 3435
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121  CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTTCTTCTGGAGCTCCA 180

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Qy	3436	GGAACCAGGCAGTGAGGCC TTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG	3495
Db	181	GGAACCAGGCAGTGAGGCC TTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG	240
Qy	3496	CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA	3555
Db	241	CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA	300
Qy	3556	CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCCTGTAGAAT	3615
Db	301	CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCCTGTAGAAT	360
Qy	3616	CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG	3675
Db	361	CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG	420
Qy	3676	GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA	3735
Db	421	GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA	480
Qy	3736	GATCTGTAAGTAGGCC TTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA	3795
Db	481	GATCTGTAAGTAGGCC TTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA	540
Qy	3796	CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT	3855
Db	541	CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT	600
Qy	3856	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	3915
Db	601	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	660
Qy	3916	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	3975
Db	661	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	720
Qy	3976	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	4035
Db	721	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	780
Qy	4036	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	4095
Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395

Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG	4634
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG	1380
Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	1500
Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814
Db	1501	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	1560
Qy	4815	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	4874
Db	1561	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	1620
Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTTCTGTTCCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTTCTGTTCCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCT	1740
Qy	4995	TTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	5054
Db	1741	TTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	5174
Db	1861	TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	1920
Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	5294

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Db      1981 TAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT 2040
Qy      5295 ATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA 5354
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041 ATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA 2100
Qy      5355 GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAA 5414
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101 GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAA 2160
Qy      5415 GGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC 5474
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161 GGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC 2220
Qy      5475 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG 5534
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG 2280
Qy      5535 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG 5594
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG 2340
Qy      5595 CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 5654
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 2400
Qy      5655 TAATGATCTTGGGTGGATCC 5674
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Db      2401 TAATGATCTTGGGTGGATCC 2420

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RESULT 11
US-10-871-708-14
; Sequence 14, Application US/10871708
; Publication No. US20050118186A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN COMPOSITIONS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.035A
; CURRENT APPLICATION NUMBER: US/10/871,708
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: 60/479,554
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Human antigen (MAGE-1) gene, complete cds
US-10-871-708-14

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Query Match          42.4%; Score 2408; DB 10; Length 2420;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60
Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375

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|||||
Db      61 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA 3435
|||||

Db      121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCC TTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
|||||

Db      181 GGAACCAGGCAGTGAGGCC TTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTTGGCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
|||||

Db      241 CACAGGGTGTGCCAGCAGTGAATGTTTGGCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCTGTAGAAT 3615
|||||

Db      301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCTGTAGAAT 360

Qy      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 3675
|||||

Db      361 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 420

Qy      3676 GGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 3735
|||||

Db      421 GGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 480

Qy      3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 3795
|||||

Db      481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 540

Qy      3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT 3855
|||||

Db      541 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT 600

Qy      3856 GCCTGCTGCCC TGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 3915
|||||

Db      601 GCCTGCTGCCC TGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 660

Qy      3916 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAAGGCTGCCAC 3975
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Db      661 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAAGGCTGCCAC 720

Qy      3976 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCTTGAGGAGGTGCCCACTGCTGGGTCAAC 4035
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Db      721 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCTTGAGGAGGTGCCCACTGCTGGGTCAAC 780

Qy      4036 AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG 4095
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Db      781 AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG 840

Qy      4096 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG 4155
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Db      841 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG 900

Qy      4156 TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGTTGGTTT 4215
|||||

Db      901 TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGTTGGTTT 960

Qy      4216 TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT 4275
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Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCCTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCCTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCACAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG	4634
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCACAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG	1380
Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	1500
Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814
Db	1501	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	1560
Qy	4815	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	4874
Db	1561	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	1620
Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTCTGTCTATTGGGTGACTTGGAGATTTATCTTTGTCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTCTGTCTATTGGGTGACTTGGAGATTTATCTTTGTCTCT	1740
Qy	4995	TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGT	5054
Db	1741	TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAT	5174
Db	1861	TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAT	1920

Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	5294
Db	1981	TAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	2040
Qy	5295	ATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	5354
Db	2041	ATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	2100
Qy	5355	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAA	5414
Db	2101	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAA	2160
Qy	5415	GGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	5474
Db	2161	GGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	2220
Qy	5475	GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	5534
Db	2221	GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	2280
Qy	5535	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGCAATG	5594
Db	2281	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGCAATG	2340
Qy	5595	CCCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTG	5654
Db	2341	CCCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTG	2400
Qy	5655	TAATGATCTTGGGTGGATCC	5674
Db	2401	TAATGATCTTGGGTGGATCC	2420

# RESULT 12

US-11-067-064-81

; Sequence 81, Application US/11067064

; Publication No. US20050142144A1

## ; GENERAL INFORMATION:

; APPLICANT: SIMARD, John, J.L.

; APPLICANT: DIAMOND, David, C.

; APPLICANT: LIU, Zheng

; TITLE OF INVENTION: EPITOPE SEQUENCES

; FILE REFERENCE: MANNK.027C2

; CURRENT APPLICATION NUMBER: US/11/067,064

; CURRENT FILING DATE: 2005-02-25

; PRIOR APPLICATION NUMBER: US 60/282,211

; PRIOR FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: US 60/337,017

; PRIOR FILING DATE: 2001-11-07

; PRIOR APPLICATION NUMBER: US 60/363,210

; PRIOR FILING DATE: 2002-03-07

; PRIOR APPLICATION NUMBER: US 10/117937

; PRIOR FILING DATE: 2002-04-04

; NUMBER OF SEQ ID NOS: 602

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 81

; LENGTH: 2420  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-067-064-81

Query Match 42.4%; Score 2408; DB 13; Length 2420;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
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Db        1 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          |||
Db       61 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 3435
          |||
Db      121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCTCAGGTCACAGAGCAGAGGATG 3495
          |||
Db      181 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCTCAGGTCACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          |||
Db      241 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCACTCCTGTAGAAT 3615
          |||
Db      301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCACTCCTGTAGAAT 360

Qy      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTTCAGGTTTTTCAG 3675
          |||
Db      361 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTTCAGGTTTTTCAG 420

Qy      3676 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGACCAAGGAGAA 3735
          |||
Db      421 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGACCAAGGAGAA 480

Qy      3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 3795
          |||
Db      481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 540

Qy      3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT 3855
          |||
Db      541 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT 600

Qy      3856 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 3915
          |||
Db      601 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 660

Qy      3916 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 3975
          |||
Db      661 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 720

Qy      3976 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 4035
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Db      721 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 780
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Qy	4036	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTACTACCATCAACTTCACTCG	4095
Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG	4634
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG	1380
Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	1500
Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814
Db	1501	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	1560
Qy	4815	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	4874
Db	1561	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	1620
Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCAC'TCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCAC'TCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCT	4994

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Db      1681 GTGTTCTCAGTAGTAGGTTTCTGTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCT 1740

Qy      4995 TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT 5054
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT 1800

Qy      5055 TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT 5114
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT 1860

Qy      5115 TTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT 5174
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861 TTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT 1920

Qy      5175 AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT 5234
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT 1980

Qy      5235 TAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT 5294
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 TAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT 2040

Qy      5295 ATGCATACCTGGATTTCCTTGCCCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAA 5354
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041 ATGCATACCTGGATTTCCTTGCCCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAA 2100

Qy      5355 GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGAA 5414
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101 GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGAA 2160

Qy      5415 GGCCCTGGGT TAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC 5474
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161 GGCCCTGGGT TAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC 2220

Qy      5475 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG 5534
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG 2280

Qy      5535 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTC AATG 5594
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTC AATG 2340

Qy      5595 CCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 5654
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 CCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 2400

Qy      5655 TAATGATCTTGGGTGGATCC 5674
      |||||||||||||||||||
Db      2401 TAATGATCTTGGGTGGATCC 2420

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RESULT 13
US-11-067-159-81
; Sequence 81, Application US/11067159
; Publication No. US20050221440A1
; GENERAL INFORMATION:
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES

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; FILE REFERENCE: MANNK.027C1
; CURRENT APPLICATION NUMBER: US/11/067,159
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 10/117937
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-067-159-81

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Query Match          42.4%; Score 2408; DB 13; Length 2420;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
          |||
Db      1 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          |||
Db      61 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA 3435
          |||
Db      121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          |||
Db      181 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          |||
Db      241 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 3615
          |||
Db      301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 360

Qy      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 3675
          |||
Db      361 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 420

Qy      3676 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 3735
          |||
Db      421 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 480

Qy      3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 3795
          |||
Db      481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 540

Qy      3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT 3855
          |||

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Db	541	CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT	600
Qy	3856	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	3915
Db	601	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	660
Qy	3916	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	3975
Db	661	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	720
Qy	3976	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCTTGAGGAGGTGCCACTGCTGGGTCAAC	4035
Db	721	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCTTGAGGAGGTGCCACTGCTGGGTCAAC	780
Qy	4036	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	4095
Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG	4634
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG	1380
Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	1500



Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814
Db	1501	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	1560
Qy	4815	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	4874
Db	1561	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	1620
Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTCTGTCTATTGGGTGACTTGGAGATTATCTTTGTCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTCTGTCTATTGGGTGACTTGGAGATTATCTTTGTCTCT	1740
Qy	4995	TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT	5054
Db	1741	TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	5174
Db	1861	TTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	1920
Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAAATTTTAAAGATAT	5294
Db	1981	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAAATTTTAAAGATAT	2040
Qy	5295	ATGCATACCTGGATTTCCTTGCCCTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAA	5354
Db	2041	ATGCATACCTGGATTTCCTTGCCCTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAA	2100
Qy	5355	GAATTCTTCCGTTCCTGTTCACTGGCTCTTTCTTCTCCATGCAC TGAGCATCTGCTTTTGGAA	5414
Db	2101	GAATTCTTCCGTTCCTGTTCACTGGCTCTTTCTTCTCCATGCAC TGAGCATCTGCTTTTGGAA	2160
Qy	5415	GGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	5474
Db	2161	GGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	2220
Qy	5475	G TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	5534
Db	2221	G TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	2280
Qy	5535	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGCAATG	5594
Db	2281	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGCAATG	2340
Qy	5595	CCCTGAGCTGGGGCATT TTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTG	5654
Db	2341	CCCTGAGCTGGGGCATT TTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTG	2400

Qy 5655 TAATGATCTTGGGTGGATCC 5674  
|||||  
Db 2401 TAATGATCTTGGGTGGATCC 2420

RESULT 14

US-11-155-288-25

; Sequence 25, Application US/11155288

; Publication No. US20060008468A1

; GENERAL INFORMATION:

; APPLICANT: Chiang, Chih-Sheng

; APPLICANT: Simard, John J.L.

; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED

; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS

; FILE REFERENCE: MANNK.050A

; CURRENT APPLICATION NUMBER: US/11/155,288

; CURRENT FILING DATE: 2005-06-17

; PRIOR APPLICATION NUMBER: 60/580,969

; PRIOR FILING DATE: 2004-06-17

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 25

; LENGTH: 2420

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-155-288-25

Query Match 42.4%; Score 2408; DB 16; Length 2420;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315  
|||||  
Db 1 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy 3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375  
|||||  
Db 61 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy 3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 3435  
|||||  
Db 121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 180

Qy 3436 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495  
|||||  
Db 181 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

Qy 3496 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555  
|||||  
Db 241 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy 3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 3615  
|||||  
Db 301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 360

Qy 3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 3675  
|||||  
Db 361 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 420

Qy 3676 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAGGAGAA 3735  
|||||

Db 421 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 480

Qy 3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 3795  
|||||

Db 481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 540

Qy 3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT 3855  
|||||

Db 541 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT 600

Qy 3856 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 3915  
|||||

Db 601 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 660

Qy 3916 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCCTGGTGTGTGTGCAGGCTGCCAC 3975  
|||||

Db 661 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCCTGGTGTGTGTGCAGGCTGCCAC 720

Qy 3976 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 4035  
|||||

Db 721 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 780

Qy 4036 AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG 4095  
|||||

Db 781 AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG 840

Qy 4096 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG 4155  
|||||

Db 841 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG 900

Qy 4156 TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTT 4215  
|||||

Db 901 TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTT 960

Qy 4216 TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT 4275  
|||||

Db 961 TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT 1020

Qy 4276 CATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA 4335  
|||||

Db 1021 CATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA 1080

Qy 4336 GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT 4395  
|||||

Db 1081 GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT 1140

Qy 4396 CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC 4455  
|||||

Db 1141 CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC 1200

Qy 4456 AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA 4515  
|||||

Db 1201 AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA 1260

Qy 4516 GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA 4575  
|||||

Db 1261 GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA 1320

Qy 4576 TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG 4634  
|||||

Db 1321 TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG 1380

Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	1500
Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814
Db	1501	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	1560
Qy	4815	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	4874
Db	1561	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	1620
Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT	1740
Qy	4995	TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	5054
Db	1741	TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	5174
Db	1861	TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	1920
Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	5294
Db	1981	TAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	2040
Qy	5295	ATGCATACCTGGATTTCCTTGCGCTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	5354
Db	2041	ATGCATACCTGGATTTCCTTGCGCTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	2100
Qy	5355	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGAA	5414
Db	2101	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGAA	2160
Qy	5415	GGCCCTGGGTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	5474
Db	2161	GGCCCTGGGTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	2220
Qy	5475	GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG	5534
Db	2221	GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG	2280

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Qy      5535 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCATG 5594
          |||
Db      2281 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCATG 2340

Qy      5595 CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 5654
          |||
Db      2341 CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 2400

Qy      5655 TAATGATCTTGGGTGGATCC 5674
          |||
Db      2401 TAATGATCTTGGGTGGATCC 2420

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RESULT 15

US-10-093-766-41

; Sequence 41, Application US/10093766

; Publication No. US20030013099A1

; GENERAL INFORMATION:

; APPLICANT: Lasek, Amy W.

; APPLICANT: Jones, David A.

; APPLICANT: Karpf, Adam R.

; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS

; FILE REFERENCE: PA-0047 US

; CURRENT APPLICATION NUMBER: US/10/093,766

; CURRENT FILING DATE: 2002-03-07

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PERL Program

; SEQ ID NO 41

; LENGTH: 2420

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; OTHER INFORMATION: Incyte ID No. US20030013099A1 410721.1

US-10-093-766-41

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Query Match          42.4%;  Score 2404.8;  DB 6;  Length 2420;
Best Local Similarity 99.9%;  Pred. No. 0;
Matches 2417;  Conservative 0;  Mismatches 2;  Indels 1;  Gaps 1;

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Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
          |||
Db      1   GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          |||
Db      61  ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTCCTGGAGCTCCA 3435
          |||
Db      121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTCCTGGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          |||
Db      181 GGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          |||
Db      241 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCTAGTCTCTAGTAAT 3615

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Db	301	CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCTAGTCTCTGTAGAAAT	360
Qy	3616	CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCTCCTTCAGGTTTTTCAG	3675
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Qy	3856	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	3915
Db	601	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	660
Qy	3916	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGTCAGGCTGCCAC	3975
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Qy	3976	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCTTGGAGGAGGTGCCCACTGCTGGGTCAAC	4035
Db	721	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCTTGGAGGAGGTGCCCACTGCTGGGTCAAC	780
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Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
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Db	1021	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCTTGT	4395
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Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
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Db 1201 AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGCCATGCTCCTGAGGA 1260

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Db 1261 GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA 1320

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Qy 5175 AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT 5234  
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Qy 5235 TAAGAGATAGTCAATTCTTGCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT 5294  
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Qy      5655 TAATGATCTTGGGTGGATCC 5674
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Db      2401 TAATGATCTTGGGTGGATCC 2420

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Search completed: August 25, 2006, 15:22:13  
Job time : 6187 secs

SCORE 1.3 BuildDate: 12/06/2005
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# SCORE Search Results Details for Application 08819669 and Search Result us-08-819-669e-8.rnpbn.

<a href="#">Score Home Page</a>	<a href="#">Retrieve Application List</a>	<a href="#">SCORE System Overview</a>	<a href="#">SCORE FAQ</a>	<a href="#">Comments / Suggestions</a>
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This page gives you Search Results detail for the Application 08819669 and Search Result us-08-819-669e-8.rnpbn.

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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2006, 13:39:22 ; Search time 856 Seconds  
(without alignments)  
10803.493 Million cell updates/sec

Title: US-08-819-669E-8  
Perfect score: 5674  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2239192 seqs, 814926892 residues

Total number of hits satisfying chosen parameters: 4478384

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA\_New:\*  
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2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
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9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq2:\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	5674	100.0	5674	8	US-11-253-240-8	Sequence 8, Appli
2	2419	42.6	2419	8	US-11-253-240-7	Sequence 7, Appli
3	2408	42.4	2420	9	US-11-323-049-18	Sequence 18, Appl
4	2408	42.4	2420	9	US-11-323-964-27	Sequence 27, Appl
5	2058.8	36.3	4157	8	US-11-253-240-9	Sequence 9, Appli
6	1762.6	31.1	4204	9	US-11-323-049-19	Sequence 19, Appl
7	1762.6	31.1	4204	9	US-11-323-964-28	Sequence 28, Appl
8	1678.8	29.6	2531	8	US-11-253-240-13	Sequence 13, Appl
9	1678.8	29.6	2531	8	US-11-253-240-14	Sequence 14, Appl
10	1504.6	26.5	2305	8	US-11-253-240-17	Sequence 17, Appl
11	1410.8	24.9	2226	8	US-11-253-240-16	Sequence 16, Appl
12	1188.2	20.9	1577	8	US-11-266-748A-87851	Sequence 87851, A
13	1188.2	20.9	1577	8	US-11-266-748A-112460	Sequence 112460,
c 14	1188.2	20.9	1577	8	US-11-266-748A-140662	Sequence 140662,
15	988.8	17.4	1640	8	US-11-253-240-11	Sequence 11, Appl
16	939.2	16.6	1000	8	US-11-266-748A-397184	Sequence 397184,
c 17	939.2	16.6	1000	8	US-11-266-748A-468230	Sequence 468230,
18	900.2	15.9	1810	8	US-11-253-240-20	Sequence 20, Appl
19	830.6	14.6	1947	8	US-11-253-240-19	Sequence 19, Appl
20	815.2	14.4	1412	8	US-11-253-240-21	Sequence 21, Appl
21	750.8	13.2	1068	8	US-11-253-240-15	Sequence 15, Appl
c 22	720.2	12.7	747	8	US-11-266-748A-212265	Sequence 212265,
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32	634.4	11.2	1000	8	US-11-266-748A-290270	Sequence 290270,
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34	634.4	11.2	1000	8	US-11-266-748A-401488	Sequence 401488,
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39	627	11.1	1000	8	US-11-266-748A-405408	Sequence 405408,
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#### ALIGNMENTS

##### RESULT 1

US-11-253-240-8

; Sequence 8, Application US/11253240

; Publication No. US20060127356A1

; GENERAL INFORMATION:

; APPLICANT: Gaugler, Batrice; Van den Eynde, BenoEt;

; van der Bruggen, Pierre; Boon-Falleur, Thierry

```

; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/253,240
; FILING DATE: 17-Oct-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/579,543
; FILING DATE: 26-May-2000
; APPLICATION NUMBER: 09/583,850
; FILING DATE:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; APPLICATION NUMBER: 07/764,365
; FILING DATE: 23-SEPTEMBER-1991
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-11-253-240-8

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Best Local Similarity 100.0%;  Pred. No. 0;
Matches 5674;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCTAGGACACCGACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCTAGGACACCGACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTTCCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTTCCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGTTCAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGTTCAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820

QY	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCCAG	2880
QY	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCCAGAG	2940
QY	2941	AGCATGGGCTGGGCCGCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
QY	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
QY	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
QY	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
QY	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACTCTTGATTGGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACTCTTGATTGGATTCTCAG	3240
QY	3241	ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
QY	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
QY	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
QY	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
QY	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
QY	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
QY	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
QY	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
QY	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCAAGGTTTCAGTTCTC	3780

Db	3721		GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTCTC	3780
Qy	3781		AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781		AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841		CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841		CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901		TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901		TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961		TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCTGGAGGAGGTGCC	4020
Db	3961		TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCTGGAGGAGGTGCC	4020
Qy	4021		CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021		CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081		CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081		CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141		GCCAAGCACCTCTTGTATCCTGGAGTCCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141		GCCAAGCACCTCTTGTATCCTGGAGTCCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201		TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201		TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261		AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261		AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321		CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321		CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381		CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTGATAATCA	4440
Db	4381		CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTGATAATCA	4440
Qy	4441		GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441		GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501		CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501		CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561		GGAGCACAGTGCTTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561		GGAGCACAGTGCTTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621		GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680



Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTTGGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Db	5401	TCTGCTTTTTGGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Qy	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Db	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Qy	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGAGGGCTCCGGGTGAGAGTG	5580
Db	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGAGGGCTCCGGGTGAGAGTG	5580

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Qy      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
        |||||||||||||||||||||||||||||||||||||||
Db      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640

Qy      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
        ||||||||||||||||||||||||||||
Db      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

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RESULT 2

US-11-253-240-7

; Sequence 7, Application US/11253240

; Publication No. US20060127356A1

; GENERAL INFORMATION:

; APPLICANT: Gaugler, Batrice; Van den Eynde, BenoEt;

; van der Bruggen, Pierre; Boon-Falleur, Thierry

; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For

; Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch

; STREET: 805 Third Avenue

; CITY: New York City

; STATE: New York

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/11/253,240

; FILING DATE: 17-Oct-2005

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/579,543

; FILING DATE: 26-May-2000

; APPLICATION NUMBER: 09/583,850

; FILING DATE:

; APPLICATION NUMBER: PCT/US92/04354

; FILING DATE: 22-MAY-1992

; APPLICATION NUMBER: 07/807,043

; FILING DATE: 12-DECEMBER-1991

; APPLICATION NUMBER: 07/764,365

; FILING DATE: 23-SEPTEMBER-1991

; APPLICATION NUMBER: 07/728,838

; FILING DATE: 9-JULY-1991

; APPLICATION NUMBER: 07/705,702

; FILING DATE: 23-MAY-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, Norman D.

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; REFERENCE/DOCKET NUMBER: LUD 5353

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; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2419 base pairs

; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-11-253-240-7
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Query Match          42.6%; Score 2419; DB 8; Length 2419;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
          |||
Db       1  GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          |||
Db       61 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 3435
          |||
Db      121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          |||
Db      181 GGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          |||
Db      241 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 3615
          |||
Db      301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 360

Qy      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 3675
          |||
Db      361 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 420

Qy      3676 GGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 3735
          |||
Db      421 GGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 480

Qy      3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCAGCTGAGGCCTCTCA 3795
          |||
Db      481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCAGCTGAGGCCTCTCA 540

Qy      3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT 3855
          |||
Db      541 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT 600

Qy      3856 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 3915
          |||
Db      601 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 660

Qy      3916 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 3975
          |||
Db      661 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 720

Qy      3976 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 4035
          |||
Db      721 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 780
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Qy	4036	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTACTACCATCAACTTCACTCG	4095
Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGCTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGCTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGG	4635
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGG	1380
Qy	4636	CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT	4695
Db	1381	CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT	1440
Qy	4696	GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTTCGCTTT	4755
Db	1441	GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTTCGCTTT	1500
Qy	4756	TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA	4815
Db	1501	TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA	1560
Qy	4816	GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGACCTTCCAGGGCCGCGTCCA	4875
Db	1561	GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGACCTTCCAGGGCCGCGTCCA	1620
Qy	4876	GCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCAG	4935
Db	1621	GCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCAG	1680

Qy	4936	TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT	4995
Db	1681	TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT	1740
Qy	4996	TTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTT	5055
Db	1741	TTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTT	1800
Qy	5056	TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTTGTT	5115
Db	1801	TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTTGTT	1860
Qy	5116	TTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGGAATA	5175
Db	1861	TTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGGAATA	1920
Qy	5176	AGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT	5235
Db	1921	AGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT	1980
Qy	5236	AAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATA	5295
Db	1981	AAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATA	2040
Qy	5296	TGCATACCTGGATTTCCCTGGCTTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAAG	5355
Db	2041	TGCATACCTGGATTTCCCTGGCTTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAAG	2100
Qy	5356	AATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAAG	5415
Db	2101	AATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAAG	2160
Qy	5416	GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG	5475
Db	2161	GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG	2220
Qy	5476	TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG	5535
Db	2221	TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG	2280
Qy	5536	GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGC	5595
Db	2281	GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGC	2340
Qy	5596	CCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTGT	5655
Db	2341	CCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTGT	2400
Qy	5656	AATGATCTTGGGTGGATCC	5674
Db	2401	AATGATCTTGGGTGGATCC	2419

RESULT 3

US-11-323-049-18

; Sequence 18, Application US/11323049

; Publication No. US2006015969A1

; GENERAL INFORMATION:

; APPLICANT: Chiang, Chih-Sheng

; APPLICANT: Simard, John J.L.

; APPLICANT: Diamond, David C.

```

; APPLICANT: Bot, Adrian Ion
; APPLICANT: Liu , Xiping
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN COMPOSITIONS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.049A
; CURRENT APPLICATION NUMBER: US/11/323,049
; CURRENT FILING DATE: 2005-12-29
; PRIOR APPLICATION NUMBER: 60/640,598
; PRIOR FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-323-049-18

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Query Match          42.4%; Score 2408; DB 9; Length 2420;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1  GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

QY      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

QY      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA 3435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA 180

QY      3436 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

QY      3496 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

QY      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCTGTAGAAT 3615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCTGTAGAAT 360

QY      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 3675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 420

QY      3676 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGACCAAGGAGAA 3735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGACCAAGGAGAA 480

QY      3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 3795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 540

QY      3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT 3855
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT 600

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Qy	3856	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	3915
Db	601	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	660
Qy	3916	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGTCAGGCTGCCAC	3975
Db	661	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGTCAGGCTGCCAC	720
Qy	3976	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCTTGGAGGAGGTGCCCACTGCTGGGTCAAC	4035
Db	721	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCTTGGAGGAGGTGCCCACTGCTGGGTCAAC	780
Qy	4036	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	4095
Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG	4634
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG	1380
Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	1500
Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814

Db	1501		1560
Qy	4815	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	4874
Db	1561	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	1620
Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTTCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTTCTGTTCATTGGGTGACTTGGAGATTTATCTTTGTTCCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTTCTGTTCATTGGGTGACTTGGAGATTTATCTTTGTTCCTCT	1740
Qy	4995	TTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	5054
Db	1741	TTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	5174
Db	1861	TTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	1920
Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	5294
Db	1981	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	2040
Qy	5295	ATGCATACCTGGATTTCCTTGCGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	5354
Db	2041	ATGCATACCTGGATTTCCTTGCGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	2100
Qy	5355	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACCTGAGCATCTGCTTTTGGAA	5414
Db	2101	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACCTGAGCATCTGCTTTTGGAA	2160
Qy	5415	GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	5474
Db	2161	GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	2220
Qy	5475	GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	5534
Db	2221	GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	2280
Qy	5535	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG	5594
Db	2281	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG	2340
Qy	5595	CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG	5654
Db	2341	CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG	2400
Qy	5655	TAATGATCTTGGGTGGATCC	5674



Db 2401 TAATGATCTTGGGTGGATCC 2420

RESULT 4

US-11-323-964-27

; Sequence 27, Application US/11323964

; Publication No. US20060159689A1

; GENERAL INFORMATION:

; APPLICANT: Chiang, Chih-Sheng

; APPLICANT: Simard, John J.L.

; APPLICANT: Diamond, David C.

; APPLICANT: Bot, Adrian Ion

; APPLICANT: Liu, Xiping

; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED

; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS

; FILE REFERENCE: MANNK.050CP1

; CURRENT APPLICATION NUMBER: US/11/323,964

; CURRENT FILING DATE: 2005-12-29

; PRIOR APPLICATION NUMBER: 11/155,288

; PRIOR FILING DATE: 2005-06-17

; PRIOR APPLICATION NUMBER: PCT/US2005/021836

; PRIOR FILING DATE: 2005-06-17

; PRIOR APPLICATION NUMBER: 60/580,969

; PRIOR FILING DATE: 2004-06-17

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 27

; LENGTH: 2420

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-323-964-27

Query Match 42.4%; Score 2408; DB 9; Length 2420;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
          |||
Db      1  GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          |||
Db      61  ACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 3435
          |||
Db      121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          |||
Db      181 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          |||
Db      241 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 3615
          |||
Db      301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 360

Qy      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTCAG 3675
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Db	361	CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTCAG	420
Qy	3676	GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACC AAGGAGAA	3735
Db	421	GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACC AAGGAGAA	480
Qy	3736	GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA	3795
Db	481	GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA	540
Qy	3796	CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT	3855
Db	541	CACACTCCCTCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT	600
Qy	3856	GCCTGCTGCCC TGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	3915
Db	601	GCCTGCTGCCC TGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	660
Qy	3916	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	3975
Db	661	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	720
Qy	3976	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	4035
Db	721	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	780
Qy	4036	AGATCCTCCCCAGAGTCCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	4095
Db	781	AGATCCTCCCCAGAGTCCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575

Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAAGTACCTGGAGTA-CG	4634
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAAGTACCTGGAGTACCG	1380
Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGAAGAGTTCGCTT	1500
Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814
Db	1501	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	1560
Qy	4815	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	4874
Db	1561	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	1620
Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTTCTGTCTATTGGGTGACTTGGAGATTATCTTTGTCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTTCTGTCTATTGGGTGACTTGGAGATTATCTTTGTCTCT	1740
Qy	4995	TTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	5054
Db	1741	TTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	5174
Db	1861	TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	1920
Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	5294
Db	1981	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	2040
Qy	5295	ATGCATACCTGGATTTCCCTTGCTTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAA	5354
Db	2041	ATGCATACCTGGATTTCCCTTGCTTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAA	2100
Qy	5355	GAATTCTTCCGTGTTCACTGGCTCTTTTCTTCTCCATGCACGTGAGCATCTGCTTTTGGAA	5414
Db	2101	GAATTCTTCCGTGTTCACTGGCTCTTTTCTTCTCCATGCACGTGAGCATCTGCTTTTGGAA	2160
Qy	5415	GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	5474
Db	2161	GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	2220

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Qy      5475 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG 5534
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Db      2221 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG 2280

Qy      5535 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG 5594
        |||
Db      2281 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG 2340

Qy      5595 CCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 5654
        |||
Db      2341 CCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 2400

Qy      5655 TAATGATCTTGGGTGGATCC 5674
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Db      2401 TAATGATCTTGGGTGGATCC 2420

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RESULT 5

US-11-253-240-9

; Sequence 9, Application US/11253240

; Publication No. US20060127356A1

; GENERAL INFORMATION:

; APPLICANT: Gaugler, Batrice; Van den Eynde, BenoEt;  
; van der Bruggen, Pierre; Boon-Falleur, Thierry  
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For  
; Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felte & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York City  
; STATE: New York  
; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
; COMPUTER: IBM  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/11/253,240  
; FILING DATE: 17-Oct-2005  
; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/579,543  
; FILING DATE: 26-May-2000  
; APPLICATION NUMBER: 09/583,850  
; FILING DATE:  
; APPLICATION NUMBER: PCT/US92/04354  
; FILING DATE: 22-MAY-1992  
; APPLICATION NUMBER: 07/807,043  
; FILING DATE: 12-DECEMBER-1991  
; APPLICATION NUMBER: 07/764,365  
; FILING DATE: 23-SEPTEMBER-1991  
; APPLICATION NUMBER: 07/728,838  
; FILING DATE: 9-JULY-1991  
; APPLICATION NUMBER: 07/705,702  
; FILING DATE: 23-MAY-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, Norman D.  
; REGISTRATION NUMBER: 30,946

```

;          REFERENCE/DOCKET NUMBER: LUD 5353
;          TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (212) 688-9200
;          TELEFAX: (212) 838-3884
;          INFORMATION FOR SEQ ID NO: 9:
;          SEQUENCE CHARACTERISTICS:
;          LENGTH: 4157 base pairs
;          TYPE: nucleic acid
;          STRANDEDNESS: single
;          TOPOLOGY: linear
;          MOLECULE TYPE: genomic DNA
;          FEATURE:
;          NAME/KEY:     MAGE-2 gene
;          SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-11-253-240-9

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Query Match          36.3%;   Score 2058.8;   DB 8;   Length 4157;
Best Local Similarity 75.3%;   Pred. No. 0;
Matches 3172;   Conservative    0;   Mismatches 837;   Indels 201;   Gaps 41;

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Qy      1351 CCCATCGCCTCCCCCATTCTGGCAGAATCCGGTT-TGCCCCTGCTCTCAACCCAGGGAAG 1409
          |||||  |||||  | ||||| |||||  || |||  | ||||| |||||
Db      1   CCCATCCAGATCCCCATCCGGGCAGAATCCGGTTCCACCCTTGCCGTGAACCCAGGGAAG 60

Qy      1410 CCCTGGTAGGCCCGATGTGAAACCACTGACTTGAACCTCACAGATCTGAGAGAAGCCAGG 1469
          |  ||  |  || |||||  ||||| |||||  ||  |  || |||  || ||
Db      61  TCACGG--GCCCGGATGTGACGCCACTGACTTGCACATTGGAGGTCAGAGGACAGCGAGA 118

Qy      1470 TTCATTTAATGGTTCTGAGGGGCGGCTTGAGATCCACTGAGGGGAGTGGTTTATAGGCTCT 1529
          |||  ---  |  |  |||||  ||||  |||  ||  |  ||||  ||  |  |||||
Db      119  TTC-----TCGCCCTGAGCAACGGCCTGACGTCGGCGGAGGGAAGCAGGCGCAGGCTCC 172

Qy      1530 GTGAGGAGGCAAGGTGAGATGCTGAGGGAGGACTGAGGAGGCACACACCCAGGTTAGATG 1589
          ||||| ||||| ||||  |||  ||||| ||||| ||||  ||  |  ||||| |||  |
Db      173  GTGAGGAGGCAAGGTAAGACGCCGAGGGAGGACTGAGGCGGGCCTCACCCAGACAGAGG 232

Qy      1590 GCCCCAAATGATCCAGTACCACCCCTGCTGCCAGCCCTGGACCACCCGGCCAGGACAGA 1649
          ||||| ||  |  |||||  |  ||  ||||| ||  |  ||||| |||||  ||  ||  |||
Db      233  GCCCCCAATTAATCCAGCGCTGCCTCTGCTGCCGGGCCTGGACCACCTGCAGGGGAAGA 292

Qy      1650 TGTCTCAG-----CTGGACCACCCCCCGTCCCGTCCCACTGCCACTTAACCCACAGGG 1702
          |||||  |||||  |  |||||  |  |  |  |||  |  ||  |||  |  ||  |||||
Db      293  CTTCTCAGGCTCAGTCGCCACCACCTCACCCGCCACCCCGCCGCTTTAACCGCAGGG 352

Qy      1703 CAATCTGTAGTCATAGCTTA-TGTGACCGGGGCAGGGTTGGTCAGGAGAGGCAGGGCCCA 1761
          |  ||||  ||  |  |||||  ||||| ||||| |||||  |||  ||  ||  |
Db      353  AACTCTGGCGTAAGAGCTTTGTGTGACCAGGGCAGGGCTGGTTAGAAGTGC----- 403

Qy      1762 GGCATCAAGGTCCAGCATCCGCCCCGATTAGGGTCAGGACCCTGGGAGGGAAGTGAAGG 1821
          |||  ||  ||||  ||  |||  ||  ||  |  ||||| |||||  |||||  |||||
Db      404  ----TCAGGGCCCAGACTCAGCCAGGAATCAAGGTGAGGACCCCAAGAGGGGACTGAGGG 459

Qy      1822 TTCCCCACCCACACCTGTCTCCTCATCTCC----- 1851
          ||||| ||  |  ||  |  ||  ||
Db      460  CAACCCACCCCTACCCTCACTACCAATCCCATCCCCAACACCAACCCACCCCATCC 519

Qy      1852 -----ACCGCCACCCCACTCACATTCCCATACTACCCCTACCCCAACCTCATCTTGT 1906
          ||  |  ||||| ||  |||  ||  |  |  ||||| ||||  ||
Db      520  CTCAAACACCAACCCACCCCAAAACCCATTCCCATCTCCTCCCCACCACCATCTGG 579

Qy      1907 CAGAAT-----CCCTGCTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCA 1956

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Db	580	CAGAAATCCGGCTTTGCCCCCTGCAATCAACCCACGGAAGCTCCGGGAATGGCGGCCAAGCA	639
Qy	1957	CTCGGATCTTGACGTCCCCATCCAGGTCTGATGGAGGGAAGGGG-----CTTGAAC	2008
Db	640	CGCGGATCCTGACGTTACATGTACGG-CTAAGGGAGGGAAGGGGTTGGGTCTCGTGAGT	698
Qy	2009	AGGGCCTCAGGGGAGCAGAGGGAGGGC-----CCTACTGCGAGATGAGGGAGGCCTCAGA	2063
Db	699	ATGGCCTTTGGGATGCAGAGGAAGGGCCAGGCCTCCTGGAAGACAGTGGAGTCCCTTAGG	758
Qy	2064	GGACCCAGCACCCCTAGGA-----CACCGCACCCCTGTCTGAGACTGAGGCTGCCAC	2114
Db	759	GGACCCAGCATGCCAGGACAGGGGGCCACTGTACCCCTGTCTCAAAC TGAGCCACCTTT	818
Qy	2115	TTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGGGTGGGACCCAGGCC	2174
Db	819	TCATTACGCCGAGGGAATCCTAGGGATGCAGACCCACTTCAGGGGGTTGGGGCCAGCCT	878
Qy	2175	TGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTTGGAATCCAGATCAG	2234
Db	879	GCGAGGAGTCAAGGGGAGGAAGAAGAGGGAGGACTGAGGGGACCTTGAGTCCAGATCAG	938
Qy	2235	TGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATGGCCCATATTTCTCTG	2294
Db	939	TGGCAACCTTGG-GCTGGGGGATCCTGGGCACAGTGGCCGAATGTGCCCGTGCTCATTG	997
Qy	2295	CATCTTTGAGGTGAC---AGGACAGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTCAAC	2350
Db	998	CACCTTCAGGGTGACAGAGAGTTGAGGGCTGTGGTCTGAGGGCTGGGACTTCAGGTACGC	1057
Qy	2351	AGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATGAGGACTGGGG	2410
Db	1058	AGAGGGAGGAATCCCAGGATCTGCCGGACCAAGGTGTGCCCCCTTCATGAGGACTCCCC	1117
Qy	2411	ATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCTTTTAGTAGCTC	2470
Db	1118	ATACCCCCGGCCCAGAAAGAAGGGATGCCACAGAGTCTGGAAGTAAATTGTTCTTAGCTC	1177
Qy	2471	TAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCACAGGCAGGAA	2530
Db	1178	TGGGGGAACCTGATCAGGGATGGCCCTAAGTGACAATCTCATTGTGTACCACAGGCAGGAG	1237
Qy	2531	GTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCTACTCATGTCA	2590
Db	1238	GTTGGGGAAACCTCAGGGAGATAAGGTGTTGGTGTAAGAGGAGCTGTCTGCTCATTTC	1297
Qy	2591	GGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGTGAGACAGACA	2650
Db	1298	GGGGGTTCCCCCTTGAGAAAGGGCAGTCCCTGGCAGGAGTAAAGATGAGTAACCCACAGG	1357
Qy	2651	AGGCATATTGGAATCCACACCCCAAGGGGTAGCCCTGGACACCTCACCCAGGA	2710
Db	1358	AGGCCATCATAACGTTACCCCTAGAACCAAGGGGTAGCCCTGGACAACGCACGTGGGG	1417
Qy	2711	T-----GTGGCTTCTTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCTCAT	2763
Db	1418	TAACAGGATGTGGCCCCCTCCTCATTGTCTTTCCAGATCTCAGGGAGTTGATGACCTTGT	1477
Qy	2764	TCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCGGTC	2823

[illegible]

Qy	3710	AGGCCACAGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAG	3769
Db	2430	AGGAGCATTG-----AAGGAGAAGATCTGTAAGTAAGCCTTTGTCAGAGCCTCCAAG	2481
Qy	3770	G TTCAG-----TTCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGG	3824
Db	2482	G TTCAGTTCAGTTCTCACCTAAGGCCTCACACACGCTCCTTCTCTCCCCAGGCCTGTGGG	2541
Qy	3825	TCTTCATTGCCCAGCTCCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGT	3884
Db	2542	TCTTCATTGCCCAGCTCCTGCCCGCACTCCTGCCTGCTGCCCTGACCAGAGTCATCATGC	2601
Qy	3885	CTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGG	3944
Db	2602	CTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAAGAAGGCCTTGAGGCCCGAGGAGAGG	2661
Qy	3945	CCCTGGGCCTGGTGTGTGTGCAGGCT-----GCCACCTCCTCCT	3983
Db	2662	CCCTGGGCCTGGTGGGTGCGCAGGCTCCTGCTACTGAGGAGCAGCAGACCCTTCTTCCT	2721
Qy	3984	CCTCTCCTCTGGTCTTGGGCACCTTGGAGGAGGTGCCCTGCTGGGTCAACAGATCCTC	4043
Db	2722	CTTCTACTCTAGTGGAAGTTACCTTGGGGGAGGTGCCTGCTGCCGACTCACCGAGTCCTC	2781
Qy	4044	CCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGC	4103
Db	2782	CCCACAGTCCTCAGGGAGCCTCCAGCTTCTCGACTACCATCAACTTACACTCTTTGGAGAC	2841
Qy	4104	AACCCAGTGAGGGTTCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGATCCTGG	4163
Db	2842	AATCCGATGAGGGCTCCAGCAACCAAGAAGAGGAGGGGCCAAGAATGTTCCCGACCTGG	2901
Qy	4164	AGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTGTTGGTTTCTGCTCC	4223
Db	2902	AGTCCGAGTTCCAAGCAGCAATCAGTAGGAAGATGGTTGAGTTGGTTCATTTCTGCTCC	2961
Qy	4224	TCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAA	4283
Db	2962	TCAAGTATCGAGCCAGGGAGCCGGTCACAAAGGCAGAAATGCTGGAGAGTGTCTCAGAA	3021
Qy	4284	ATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGACGCTGGTCT	4343
Db	3022	ATTGCCAGGACTTCTTTCCCGTGATCTTCAGCAAAGCCTCCGAGTACTTGACGCTGGTCT	3081
Qy	4344	TTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCTTGTACCTGCC	4403
Db	3082	TTGGCATCGAGGTGGTGAAGTGGTCCCCATCAGCCACTTGTACATCCTTGTACCTGCC	3141
Qy	4404	TAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCC	4463
Db	3142	TGGGCCTCTCCTACGATGGCCTGCTGGGCGACAATCAGGTCATGCCCAAGACAGGCTTCC	3201
Qy	4464	TGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCT	4523
Db	3202	TGATAATCGTCCTGGCCATAATCGCAATAGAGGGCGACTGTGCCCTGAGGAGAAAAATCT	3261
Qy	4524	GGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCATGGGGAGC	4583
Db	3262	GGGAGGAGCTGAGTATGTTGGAGGTGTTGAGGGGAGGGAGGACAGTGTCTTCGCACATC	3321



Qy 4584 CCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGC 4642  
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 Db 3322 CCAGGAAGCTGCTCATGCAAGATCTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGC 3381

Qy 4643 CGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCA 4702  
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 Db 3382 CCGGCAGTGATCCTGCATGCTACGAGTTCCTGTGGGGTCCAAGGGCCCTCATTTGAAACCA 3441

Qy 4703 GCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTCTTCC 4762  
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 Db 3442 GCTATGTGAAAGTCCTGCACCATACTAAAGATCGGTGGAGAACCTCACATTTCTTACC 3501

Qy 4763 CATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAG 4822  
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 Db 3502 CACCCCTGCATGAACGGGCTTTGAGAGAGGGAGAAGAGTGAGTCTCAGCACATGTTGCAG 3561

Qy 4823 CCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTT 4882  
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 Db 3562 CCAGGGCCAGTGGGAGGGGGTCTGGGCCAGTGCACCTTCCAGGGCCCATCCATTAGCTT 3621

Qy 4883 CCCCTGCCTCGTGTGACATGAGGCCCATTCCTT--CACTCTGAAGAGAGCGGTCAGTGTTC 4940  
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 Db 3622 CCACTGCCTCGTGTGATATGAGGCCCATTCCTGCCTCTTTGAAGAGAGCAGTCAGCATTC 3681

Qy 4941 TCAGTAGTAGGTTTCTGTCTATTGGGTGACTTGGAGATTTATCTTTGTCTCTTTTGGGA 5000  
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 Db 3682 TTAGCAGTGAGTTTCTGTCTGTTGGATGACTTTGAGATTTATCTTTCTTCTCTGTTGGA 3741

Qy 5001 ATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGTTTATGA 5060  
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 Db 3742 ATTGTTCAAATG-TTCCTTTTAAACAAATGGTTGGATGAACCTCAGCATCCAAGTTTATGA 3800

Qy 5061 ATGACAGCAGTCACAC--AGTTCTGTGTATATAGTTTAAAGGGTAAGAGTCTTGTGTTTTA 5118  
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 Db 3801 ATGACAGTAGTCACACATAGTGCTGTTTATATAGTTTAGGGGTAAGAGTCCTGTTTTTTA 3860

Qy 5119 TTCAGATTGGGAAATCCATTCTATTTTGTGAATTG--GGATAATAACAGCAGTGGAATAA 5176  
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 Db 3861 TTCAGATTGGGAAATCCATTCCATTTTGTGAGTTGTACATAATAACAGCAGTGGAATAT 3920

Qy 5177 GTACTTAGAAATGT----GAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAA 5232  
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 Db 3921 GTATTTGCCTATATTGTGAACGAATTAGCAGTAAATACATGATACAAGGAAC----- 3973

Qy 5233 ATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGAT 5292  
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 Db 3974 -TCAAAGATAGTTAATTCTTGCCCTTATACCTCAGTCTATTATGTAAAA---TAAAAAT 4029

Qy 5293 ATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAATCTGAATA 5352  
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 Db 4030 ATGTGTA-----TGTTTTGCTTCTTTGAGAATGCAAAGAAATTAATCTGAATA 4080

Qy 5353 AAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGG 5412  
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 Db 4081 ---AATTCTTCCTGTTCACTGGCTCATTTCTTTACCATTCACTCAGCATCTGCTCTGTGG 4137

Qy 5413 AAGGCCCTGG 5422  
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 Db 4138 AAGGCCCTGG 4147

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RESULT 6
US-11-323-049-19
; Sequence 19, Application US/11323049
; Publication No. US20060159694A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; APPLICANT: Diamond, David C.
; APPLICANT: Bot, Adrian Ion
; APPLICANT: Liu , Xiping
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN COMPOSITIONS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.049A
; CURRENT APPLICATION NUMBER: US/11/323,049
; CURRENT FILING DATE: 2005-12-29
; PRIOR APPLICATION NUMBER: 60/640,598
; PRIOR FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 4204
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-323-049-19

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Qy	2790	AGGGACCCCCATCTGGTCTAAAGACAGAGCGGTCCCAGGATCTGCCATGCGTTCGGGTGA	2849
Db	1365	AGGGGCCCTATGTGGTGGACAGATGCAGTGGTCCTAGGATCTGCCAAGCATCCAGGTGA	1424
Qy	2850	GGAACATGAGGGGAGGACTGAGGGTACCCAGGACCAGAACACTGA-GGGAGACTGCACAG	2908
Db	1425	AGAGACTGAGGGGAGGATTGAGGGTACCCCTGGGACAGAATGCGGACTGGGGGCCCCATAA	1484
Qy	2909	AAATCAGCCCTGCCCCTGCTGTCACCCAGAGAGCATGGGCTGGGCCGTCTGCCGAGGTC	2968
Db	1485	AAATCTGCCCTGCTCCTGCTGTTACCTCAGAGAGCCTGGGCAGGGCTGTCAGCTGAGGTC	1544
Qy	2969	CTTCCGTTATCCTGGGATCATTGATGTCAGGGACGGGGAGGCCTTGGTCTGAGAAGGCTG	3028
Db	1545	CCTCCATTATCCTAGGATCACTGATGTCAGGGAAGGGGAAGCCTTGGTCTGAGGGGGCTG	1604
Qy	3029	CGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACCAAGC	3088
Db	1605	CACTCAGGGCAGTAGAGGGAGGCTCTCAGACCCTACTAGGAGTGAGGTGAGGACCAAGC	1664
Qy	3089	GGGCACCTCACCCAGGACACATTAATTCCAATGAATTTTGATATCTCTTGCTG-CCCTTC	3147
Db	1665	AGTCTCCTCACCCAGGGTACATGGACTTCAATAAATTTGGACATCTCTCGTTGTCCTTTC	1724
Qy	3148	CCCAAGGACCTAGGCACGTGTGGCCAGATGTTTGTCCTCCTGTCCTTCCATTTCCTTAT	3207
Db	1725	CGGGAGGACCTGGGAATGTATGGCCAGATGTGGGTCCCCTCATGTTTTTCTGTACCATAT	1784
Qy	3208	CATGGATGTGAACTCTTG--ATTTGGATTCTCAGACCAGCAAAAGGGCAGGATCCAGGC	3265
Db	1785	CAGGTATGTGAGTTCTTGACATGAGAGATTCTCAGGCCAGCAGAAGGGAGGGAT-TAGGC	1843

Qy 3266 CCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCCACTGCATGAG 3325  
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 Db 1844 CCTATAAGGAGAAAGGTGAGGGCCCTGAGTGAGCACAGAGGGGATCCTCCACCCAGTAG 1903

Qy 3326 AGTGGGGATGTCACAGAGTCCAGCCCACCTCCTGGTAGCACTGAGAAGCCAGGGCTGTG 3385  
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 Db 1904 AGTGGGGACCTCACAGAGTCTGGCCAACCTCCTGACAGTTCTGGGAATCCGTGGCTGCG 1963

Qy 3386 CTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTC-----CTGGAGCTCCAGGA 3438  
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 Db 1964 TTTGCTGTCTGCACATTGGGGGGCCCGTGGATTCTCTCTCCAGGAATCAGGAGCTCCAGGA 2023

Qy 3439 ACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATGCAC 3498  
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 Db 2024 ACAAGGCAGTGAGGACTTGGTCTGAGGCAGTGTCTCAGGTCACAGAGTAGAGGGGGCTC 2083

Qy 3499 AGGGTGTGCCAGCAGTGAATGTTTGCCTTGAATGCACACCAAGGGCCCCACCTGCCACAG 3558  
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 Db 2084 AGATAGTGCCAACGGTGAAGGTTTGCCTTGGATTCAAACCAAGGGCCCCACCTGCCCCAG 2143

Qy 3559 GACACATAGGACTCCACAGAGTCTGGCCTCA-CCTCCCTACTGTCAGTCTGTAGAATCG 3617  
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 Db 2144 AACACAT-GGACTCCAGAGCGCCTGGCCTCACCTCAATACTTTCAGTCTTGCAGCCTCA 2202

Qy 3618 ACCTCTGCTGGCCGGCTGTACCCTGA-GTACCCTCTCACTTCCTCCTCAGGTTTTCAGG 3676  
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 Db 2203 GCATGCGCTGGCCGGATGTACCCTGAGGTGCCCTCTCACTTCCTCCTCAGGTTCTGAGG 2262

Qy 3677 GGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAGGAGAAG 3736  
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 Db 2263 GGACAGGCTGACCTGGAGGACCAGAGGCCCCCGGAGGAGCACTG-----AAGGAGAAG 2315

Qy 3737 ATCTGTAAGTAGGCCTTTGTAGAGTCTCCAAGG-----TTCAGTTCTCAGCTGAGGCCCT 3791  
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 Db 2316 ATCTGTAAGTAAGCCTTTGTAGAGCCTCCAAGGTTCCATTTCAGTACTCAGCTGAGGTCT 2375

Qy 3792 CTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCCACAC 3851  
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 Db 2376 CTCACATGCTCCCTCTCTCCCCAGGCCAGTGGGTCTTCATTGCCCAGCTCCTGCCCCACAC 2435

Qy 3852 TCCTGCCTGCTGCCCCGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCA 3911  
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 Db 2436 TCCCGCCTGTTGCCCTGACCAGAGTCATCATGCCTCTTGAGCAGAGGAGTCAGCACTGCA 2495

Qy 3912 AGCCTGAGGAAGCCCTTGTAGGCCCAACAAGAGGCCCTGGGCCCTGGTGTGTGTGCAGGCT- 3970  
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 Db 2496 AGCCTGAAGAAGGCCCTTGTAGGCCCGAGGAGAGGCCCTGGGCCCTGGTGGGTGCGCAGGCTC 2555

Qy 3971 -----GCCACCTCCTCCTCCTCCTCCTGCTGCTGGGCACCTGG 4010  
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 Db 2556 CTGCTACTGAGGAGCAGGAGGCTGCCTCCTCCTCTTCTACTCTAGTTGAAGTCACCTGG 2615

Qy 4011 AGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCCTCAGGGAGCCTCCGCCT 4070  
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 Db 2616 GGGAGGTGCCCTGCTGCCGAGTCACCAGATCCTCCCCAGAGTCCCTCAGGGAGCCTCCAGCC 2675

Qy 4071 TTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTG 4130  
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 Db 2676 TCCCACTACCATGAACACCTCTCTGGAGCCAATCCTATGAGGACTCCAGCAACCAAG 2735

Qy 4131 AAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTA 4190

Db	2736	 AAGAGGAGGGGCCAAGCACCTTCCCTGACCTGGAGTCCGAGTTCCAAGCAGCACTCAGTA	2795
Qy	4191	AGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCA	4250
Db	2796	 GGAAGGTGGCCGAGTTGGTTCATTTTCTGCTCCTCAAGTATCGAGCCAGGGAGCCGGTCA	2855
Qy	4251	CAAAGGCAGAAATGCTGGAGAGTGCATCAAAAATTACAAGCACTGTTTTCTGAGATCT	4310
Db	2856	 CAAAGGCAGAAATGCTGGGGAGTGTGCTCGGAAATTGGCAGTATTTCTTTCTGTGATCT	2915
Qy	4311	TCGGCAAAGCCTCTGAGTCCCTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACC	4370
Db	2916	 TCAGCAAAGCTTCCAGTTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACC	2975
Qy	4371	CCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGG	4430
Db	2976	 CCATCGGCCACTTGTACATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGG	3035
Qy	4431	GTGATAATCAGATCATGCCCCAAGACAGGCTTCCTGATAATTGTCTGGTCATGATTGCAA	4490
Db	3036	 GTGACAATCAGATCATGCCCCAAGGCAGGCCTCCTGATAATCGTCTCGCCATAATCGCAA	3095
Qy	4491	TGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGT	4550
Db	3096	 GAGAGGGCGACTGTGCCCTGAGGAGAAAATCTGGGAGGAGCTGAGTGTGTTAGAGGTGT	3155
Qy	4551	ATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGG	4610
Db	3156	 TTGAGGGGAGGGAAGACAGTATCTTTGGGGGATCCCAAGAAGCTGCTCACCCAACATTTCG	3215
Qy	4611	TGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGT	4669
Db	3216	 TGCAGGAAAAC TACCTGGAGTACCGGCAGGTCCCCGGCAGTGATCCTGCATGTTATGAAT	3275
Qy	4670	TCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGA	4729
Db	3276	 TCCTGTGGGGTCCAAGGGCCCTCGTTGAAACCAGCTATGTGAAAGTCCTGCACCATATGG	3335
Qy	4730	TCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAG	4789
Db	3336	 TAAAGATCAGTGGAGGACCTCACATTTCTTACCCACCCCTGCATGAGTGGGTTTTGAGAG	3395
Qy	4790	AGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGC	4849
Db	3396	 AGGGGAAGAGTGAGTCTGAGCACGAGTTGCAGCCAGGGCCAGTGGGAGGGGGTCTGGGC	3455
Qy	4850	CAGTGCACCTTCCAGGGCCGCTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCCA	4909
Db	3456	 CAGTGCACCTTCCGGGGCCGATCCCTTAGTTTCCACTGCCTCCTGTGACGTGAGGCCCCA	3515
Qy	4910	TTCTTCACTC--TGAAGAGAGCGGTGAGTGTCTCAGTAGTAGGTTTCTGTTCATTGGG	4967
Db	3516	 TTCTTCACTCTTTGAAGCAGCAGTCAGCATTCCTTAGTAGTGGGTTTCTGTTCGTGTTGGA	3575
Qy	4968	TGACTTGGAGATTTATCTTTGTCTCTTTTGAATTGTTCAAATGTTTTTTTAAAGGGA	5027
Db	3576	 TGACTTTGAGATTATCTTTGTTTCTGTTGGAGTTGTTCAAATG-TTCCTTTTAACGGA	3634
Qy	5028	TGGTTGAATGAACCTCAGCATCCAAGTTTATGAATGACAGCAGTCACAC--AGTTCGTG	5085

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Db      3635 TGGTTGAATGAGCGTCAGCATCCAGGTTTATGAATGACAGTAGTCACACATAGTGCTGTT 3694
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Db      3695 TATATAGTTTAGGAGTAAGAGTCTTGTTTTTTACTCAAATTGGGAAATCCATTCCATTTT 3754
Qy      5146 GTGAATTGGG--ATAATAACAGCAGTGGAATAAGTA----CTTAGAAATGTGA-AAAATG 5198
        |||||
Db      3755 GTGAATTGTGACATAATAATAGCAGTGGTAAAAGTATTTGCTTAAATTTGTGAGCGAATT 3814
Qy      5199 AGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTT 5258
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Db      3815 AGCAATAACATACATGAGAT----AACTCAAGAAATCAAAGATAGTTGATTCTTGCCCTT 3870
Qy      5259 ATACCTCAGTCTATTCTGTAAAATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCT 5318
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Db      3871 GTACCTCAATCTATTCTGTAAAA---TTAAACAAATATGCAAACCAGGATTTCCCTTGACT 3927
Qy      5319 TCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAGAATTCTTCCTGTTCAGTGGCTCT 5378
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Db      3928 TCTTTGAGAATGCAAGCGAAATTAAATCTGAATAAATAATTCTTCCTCTTCACTGGCTCG 3987
Qy      5379 TTTCTTCTCCATGCACCTGAGCATCTGCTTTTTTGGAGGCCCTGGGTTAGTAGTGAGATG 5438
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Db      3988 TTTCTTTTCCGTTCACCTCAGCATCTGCTCTGTGGAGGCCCTGGGTTAGTAGTGGGGATG 4047
Qy      5439 CTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGTCAGGAGCTGCAGTCAC 5498
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Db      4048 CTAAGGTAAGCCAGACTCACGCCTACCCATAGGGCTGTAGAGCCTAGGACCTGCAGTCAT 4107
Qy      5499 GTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGG 5558
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Db      4108 ATAATTAAGGTGGTGAGAAAGTCTGTAAAGATGTAGAGGAAATGTAAGAGAGGGGTGAGGG 4167
Qy      5559 TGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCATGC 5595
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Db      4168 TGTGGCGCTCCGGGTGAGAGTAGTGGAGTGTCAGTGC 4204

```

# RESULT 7

US-11-323-964-28

; Sequence 28, Application US/11323964

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## ; GENERAL INFORMATION:

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; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED

; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS

; FILE REFERENCE: MANNK.050CP1

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Db 2084 AGATAGTGCCAACGGTGAAGGTTTGCCTTGGATTCAAACCAAGGGCCCCACCTGCCCCAG 2143

Qy 3559 GACACATAGGACTCCACAGAGTCTGGCCTCA-CCTCCCTACTGTCAGTCCTGTAGAATCG 3617  
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Db 2144 AACACAT-GGACTCCAGAGCGCTGGCCTCACCTCAATACTTTCAGTCCTGCAGCCTCA 2202

Qy 3618 ACCTCTGCTGGCCGGCTGTACCCTGA-GTACCCTCTCACTTCCTCCTTCAGGTTTTCAGG 3676  
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Db 2203 GCATGCGCTGGCCGGATGTACCCTGAGGTGCCCTCTCACTTCCTCCTTCAGGTTCTGAGG 2262

Qy 3677 GGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAAG 3736  
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Db 2263 GGACAGGCTGACCTGGAGGACCAGAGGCCCGGAGGAGCACTG-----AAGGAGAAG 2315

Qy 3737 ATCTGTAAGTAGGCCTTTGTAGAGTCTCCAAGG-----TTCAGTTCTCAGCTGAGGCCT 3791  
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Db 2316 ATCTGTAAGTAAGCCTTTGTAGAGCCTCCAAGGTTCCATTCACTCAGTCTCAGCTGAGGTCT 2375

Qy 3792 CTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACAC 3851  
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Db 2376 CTCACATGCTCCCTCTCTCCCCAGGCCAGTGGGTCTCCATTGCCCAGCTCCTGCCCACAC 2435

Qy 3852 TCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCA 3911  
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Db 2436 TCCCGCCTGTTGCCCTGACCAGAGTCATCATGCCTCTTGAGCAGAGGAGTCAGCACTGCA 2495

Qy 3912 AGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTCAGGCT- 3970  
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Db 2496 AGCCTGAAGAAGGCCCTTGAGGCCCGAGGAGAGGCCCTGGGCCTGGTGGGTGCGCAGGCTC 2555

Qy 3971 -----GCCACCTCCTCCTCCTCCTCTGGTCCTGGGCACCTGG 4010  
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Db 2556 CTGCTACTGAGGAGCAGGAGGCTGCCTCCTCCTCTTCTACTCTAGTTGAAGTCACCCTGG 2615

Qy 4011 AGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCT 4070  
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Db 2616 GGGAGGTGCCCTGCTGCCGAGTCACCAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCAGCC 2675

Qy 4071 TTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGTTCCAGCAGCCGTG 4130  
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Db 2676 TCCCACTACCATGAATACCTCTCTGGAGCCAATCCTATGAGGACTCCAGCAACCAAG 2735

Qy 4131 AAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTA 4190  
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Db 2736 AAGAGGAGGGGCCAAGCACCTTCCCTGACCTGGAGTCCGAGTTCCAAGCAGCACTCAGTA 2795

Qy 4191 AGAAGGTGGCTGATTTGGTTGGTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCA 4250  
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Db 2796 GGAAGGTGGCCGAGTTGGTTCATTTCTGCTCCTCAAGTATCGAGCCAGGGAGCCGGTCA 2855

Qy 4251 CAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCCTGAGATCT 4310  
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Db 2856 CAAAGGCAGAAATGCTGGGGAGTGTGTCGGAATTGGCAGTATTTCTTTCCTGTGATCT 2915

Qy 4311 TCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACC 4370  
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Db 2916 TCAGCAAAGCTTCCAGTTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACC 2975

Qy 4371 CCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGG 4430  
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Db 2976 CCATCGGCCACTTGTACATCTTGGCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGG 3035

Qy	4431	GTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAA	4490
Db	3036	GTGACAATCAGATCATGCCCAAGGCAGGCTTCCTGATAATCGTCCTGGCCATAATCGCAA	3095
Qy	4491	TGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGT	4550
Db	3096	GAGAGGGCGACTGTGCCCTGAGGAGAAATCTGGGAGGAGCTGAGTGTGTTAGAGGTGT	3155
Qy	4551	ATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCAAGATTTGG	4610
Db	3156	TTGAGGGGAGGGAAGACAGTATCTTGGGGGATCCCAAGAAGCTGCTCACCAACATTTTCG	3215
Qy	4611	TGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGT	4669
Db	3216	TGCAGGAAAAC TACCTGGAGTACCGGCAGGTCCCCGGCAGTGATCCTGCATGTTATGAAT	3275
Qy	4670	TCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGA	4729
Db	3276	TCCTGTGGGGTCCAAGGGCCCTCGTTGAAACCAGCTATGTGAAAGTCCTGCACCATATGG	3335
Qy	4730	TCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAG	4789
Db	3336	TAAAGATCAGTGGAGGACCTCACATTTCTTACCCACCCCTGCATGAGTGGGTTTTGAGAG	3395
Qy	4790	AGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGC	4849
Db	3396	AGGGGGAAGAGTGAGTCTGAGCACGAGTTGCAGCCAGGGCCAGTGGGAGGGGGTCTGGGC	3455
Qy	4850	CAGTGCACCTTCCAGGGCCGCTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCA	4909
Db	3456	CAGTGCACCTTCCGGGGCCGCATCCCTTAGTTTCCACTGCCTCCTGTGACGTGAGGCCCA	3515
Qy	4910	TTCTTCACTC--TGAAGAGAGCGGTCAGTGTCTCTCAGTAGTAGGTTTCTGTCTATTGGG	4967
Db	3516	TTCTTCACTCTTTGAAGCGAGCAGTCAGCATTCCTTAGTAGTGGGTTTCTGTCTGTGTTGGA	3575
Qy	4968	TGACTTGGAGATTTATCTTTGTCTCTTTTGGAAATTGTTCAAATGTTTTTTTAAAGGGA	5027
Db	3576	TGACTTTGAGATTATCTTTGTTTCTCTGTTGGAGTTGTTCAAATG-TTCCTTTTAACGGA	3634
Qy	5028	TGGTTGAATGAAC TTCAGCATCCAAGTTTATGAATGACAGCAGTCACAC--AGTTCGTG	5085
Db	3635	TGGTTGAATGAGCGTCAGCATCCAGGTTTATGAATGACAGTAGTCACACATAGTGCTGTT	3694
Qy	5086	TATATAGTTTAAAGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTT	5145
Db	3695	TATATAGTTTAGGAGTAAGAGTCTTGTTTTTTACTCAAATTGGGAAATCCATTCCATTTT	3754
Qy	5146	GTGAATTGGG--ATAATAACAGCAGTGGAAATAAGTA----CTTAGAAATGTGA-AAAATG	5198
Db	3755	GTGAATTGTGACATAATAATAGCAGTGGTAAAAGTATTTGCTTAAAATGTGAGCGAATT	3814
Qy	5199	AGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCT	5258
Db	3815	AGCAATAACATACATGAGAT----AACTCAAGAAATCAAAGATAGTTGATTCTTGCCCT	3870
Qy	5259	ATACCTCAGTCTATTCTGTAAAAATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCT	5318
Db	3871	GTACCTCAATCTATTCTGTAAAA---TTAAACAAATATGCAAACCAGGATTTTCCTTGACT	3927



Qy	5319	TCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCT	5378
Db	3928	TCTTTGAGAATGCAAGCGAAATTAAATCTGAATAAATAATTCTTCCTCTTCACTGGCTCG	3987
Qy	5379	TTTCTTCTCCATGCCTGAGCATCTGCTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATG	5438
Db	3988	TTTCTTTTCCGTTCACTCAGCATCTGCTCTGTGGGAGGCCCTGGGTTAGTAGTGGGGATG	4047
Qy	5439	CTAAGGTAAGCCGAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCAC	5498
Db	4048	CTAAGGTAAGCCGAGACTCACGCCTACCCATAGGGCTGTAGAGCTTAGGACCTGCAGTCAT	4107
Qy	5499	GTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGG	5558
Db	4108	ATAATTAAGGTGGTGAGAAGTCTGTAAAGATGTAGAGGAAATGTAAGAGAGGGGTGAGGG	4167
Qy	5559	TGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCATGC	5595
Db	4168	TGTGGCGCTCCGGGTGAGAGTAGTGGAGTGTCAGTGC	4204



Db 539 ACATGCTCCCTCTCTCCGTAGGCCTGTGGGTCCCCATTGCCAGCTTTTGCCTGCACTCT 598

Qy 3855 TGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGC 3914  
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Db 599 TGCCTGCTGCCCTGACCAGAGTCATCATGTCTTCTGAGCAGAAGAGTCAGCACTGCAAGC 658

Qy 3915 CTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCA 3974  
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Db 659 CTGAGGAAGGCGTTGAGGCCCAAGAAGAGGCCCTGGGCCTGGTGGGTGCACAGGCTCCTA 718

Qy 3975 C-----CTCCTCCTCCTCCTCCTGTCCTGGGCACCCCTGG 4010  
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Db 719 CTACTGAGGAGCAGGAGGCTGTGTCTCCTCCTCCTCCTCCTGTCCTGGCACCCTGG 778

Qy 4011 AGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCT 4070  
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Db 779 AGGAAGTGCCTGCTGTGAGTCAGCAGGTCCTCCCCAGAGTCCTCAGGGAGCCTCTGCCT 838

Qy 4071 TTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCAGCAGCCGTG 4130  
 |

Db 839 TACCACTACCATCAGCTTCACTTGCTGGAGGCAACCAATGAGGGTTCAGCAGCCAAG 898

Qy 4131 AAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTA 4190  
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Db 899 AAGAGGAGGGGCCAAGCACCTCGCCTGACGAGAGTCCTTGTTCGAGAAGCACTCAGTA 958

Qy 4191 AGAAGGTGGCTGATTGGTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCA 4250  
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Db 959 ACAAGGTGGATGAGTTGGCTCATTTTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCA 1018

Qy 4251 CAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTGAGATCT 4310  
 |||||

Db 1019 CAAAGGCAGAAATGCTGGAGAGAGTCATCAAAAATTACAAGCGCTGCTTTCTGTGATCT 1078

Qy 4311 TCGGCAAAGCCTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACC 4370  
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Db 1079 TCGGCAAAGCCTCCGAGTCCCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACC 1138

Qy 4371 CCACCGGCCACTCCTATGTCTTGTACCTGCCTAGGTCCTCCTATGATGGCCTGCTGG 4430  
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Db 1139 CCGCCAGCAACACCTACACCCTTGTCACCTGCCTGGGCCTTTCCTATGATGGCCTGCTGG 1198

Qy 4431 GTGATAATCAGATCATGCCCAAGACAGGCTTCTGATAATTGTCCTGGTCATGATTGCAA 4490  
 ||

Db 1199 GTAATAATCAGATCTTTCCCAAGACAGGCCTTCTGATAATCGTCCTGGGCACAATTGCAA 1258

Qy 4491 TGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGT 4550  
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Db 1259 TGGAGGGCGACAGCGCTCTGAGGAGGAAATCTGGGAGGAGCTGGGTGTGATGGGGGTGT 1318

Qy 4551 ATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGG 4610  
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Db 1319 ATGATGGGAGGGAGCACACTGTCTATGGGGAGCCCAGGAACTGCTCACCCAAGATTGGG 1378

Qy 4611 TGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGT 4669  
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Db 1379 TGCAGGAAAACCTACCTGGAGTACCGGCAGGTACCCGGCAGTAATCCTGCGCGCTATGAGT 1438

Qy 4670 TCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGA 4729  
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Db 1439 TCCTGTGGGGTCCAAGGGCTCTGGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGG 1498

Qy	4730	TCAAGGTCAGTGCAGAGTTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAG	4789
Db	1499	TCAGGGTCAATGCAAGAGTTTCGCATTGCCATCCCATCCCTGCGTGAAGCAGCTTTGTTAG	1558
Qy	4790	AGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGG----GGACT	4845
Db	1559	AGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAGGGCTGTGGGGAAGGGGCAGGGCT	1618
Qy	4846	GGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGG	4905
Db	1619	GGGCCAGTGCATCTAACA--GCCCTGTGCAGCAGCTTCCCTTGCCTCGTGTAAACATGAGG	1676
Qy	4906	CCCATTCTTCACTC----TGAAGAGAGCGGTCAAGTGTCTCAGTAGTAGGTTTCTGTCT	4961
Db	1677	CCCATTCTTCACTCTGTTTGAAGAAAATAGTCAAGTGTCTTCTAGTAGTGGGTTTCTATTTT	1736
Qy	4962	ATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTT	5021
Db	1737	GTTGGATGACTTGGAGATTTATCTCTGTTTCCCTTTTACAATTGTTGAAATG--TTCCTTTT	1795
Qy	5022	AAGGGATGGTTGAATGAACCTTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTC	5081
Db	1796	AATGGATGGTTGAATTAACCTTCAGCATCCAAGTTTATGAATCGTAGTTAACGTATATTGC	1855
Qy	5082	TGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTA	5141
Db	1856	TGTTAATATAGTTTAGGAGTAAGAGTCTTGTTTTTTATTTCAGATTGGGAAATCCGTTCTA	1915
Qy	5142	TTTTGTGAATTGGG---ATAATAACAGCAGTGAATAAGTACTTAGAAATGTGAAAAATG	5198
Db	1916	TTTTGTGAATTGGGACATAATAACAGCAGTGGAGTAAGTATTTAGAAGTGTG---AATT	1972
Qy	5199	AGCAGTAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTT	5258
Db	1973	CACCGTGAAATAGGTGAGAT-----AAATTAAAAGATACTTAATTCCCGCCTT	2020
Qy	5259	ATACCTCAGTCTATTCTGTAAAAATTTTAAAGATATATGCATACCTGGATTTCCTTGGCT	5318
Db	2021	ATGCCTCAGTCTATTCTGTAAAAATTTAAAAATATATATGCATACCTGGATTTCCTTGGCT	2080
Qy	5319	TCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCT	5378
Db	2081	TC---GTGAATGTAAGAGAAATTAAATCTGAATAAATAATTCTTTCTGTAACTGGCTCA	2137
Qy	5379	TTTCTTCTCCATGCACTGAGCATCTGCTTTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATG	5438
Db	2138	TTTCTTCTCTATGCACTGAGCATCTGCTCTGTGGAAGGCCCAGGATTAGTAGTGGAGATA	2197
Qy	5439	CTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCAC	5498
Db	2198	CTAGGGTAAGCCAGACACACACCTACCGATAGGGTATTAAGAGTCTAGGAGCGCGGTCAT	2257
Qy	5499	GTAATCGAGGTGGCAAGATGTCTCTTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGG	5558
Db	2258	ATAATTAAGGTGACAAGATGTCTCTAAGATGTAGGGGAAAAGT----AACGAGTGTGGG	2313
Qy	5559	TGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCT	5618
Db	2314	TATGGGGCTCCAGGTGAGAGTGGTGGGTGTAATTCCTGTG--TGGGGCTTTTGGGCT	2372



; SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-11-253-240-14

Query Match 29.6%; Score 1678.8; DB 8; Length 2531;  
Best Local Similarity 84.4%; Pred. No. 0;  
Matches 2074; Conservative 0; Mismatches 317; Indels 65; Gaps 14;

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Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
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Db       1  GGATCCAGGCCCTGCCTGGAGAAATGTGAGGGCCCTGAGTGAACACAGTGGGGATCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          |||
Db      61  ACTCCATGAGAGTGGGGACCTCACAGAGTCCAGCCTACCCTCTTGATGGCACTGAGGGAC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 3435
          |
Db     121  CGGGGCTGTGCTTACAGTCTGCACCCTAAGGGCCCATGGATTCTCTCCTAGGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCCTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
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Db     181  GGAACAAGGCAGTGAGGCCCTGGTCTGAGACAGTGTCTCAGGTTACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          |||||
Db     241  CACAGGCTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCTGTAGAAT 3615
          ||
Db     301  CAAGACACATAGGACTCCAAAGAGTCTGGCCTCACCTCCCTACCATCAATCCTGCAGAAT 360

Qy      3616 CGACCTCTGCTGGCCGGCTGTACCCTGA-GTACCCTCTCACTTCCTCCTTCAGGTTTTCA 3674
          |||||
Db     361  CGACCTCTGCTGGCCGGCTATACCCTGAGGTGCTCTCTCACTTCCTCCTTCAGGTTCTGA 420

Qy      3675 GGGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGA 3734
          |
Db     421  GCAGACAGGCCAACC--GGAGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGA 478

Qy      3735 AGATCTGTAAGTAGGCCTTTGTGTAGAGTCTCCAAGGTTCA GTTCTCAGCTGAGGCCCTCTC 3794
          |||||
Db     479  AGATCTGTAAGTAAGCCTTTGTGTAGAGCCTCTAAGATTG GTTCTCAGCTGAGGTCTCTC 538

Qy      3795 ACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCC 3854
          |||
Db     539  ACATGCTCCCTCTCTCCGTAGGCCTGTGGGTCCCCATTGCCCAGCTTTTGCTGCACTCT 598

Qy      3855 TGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGC 3914
          |||||
Db     599  TGCCTGCTGCCCTGAGCAGAGTCATCATGTCTTCTGAGCAGAAGAGTCAGCACTGCAAGC 658

Qy      3915 CTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCA 3974
          |||||
Db     659  CTGAGGAAGGCGTTGAGGCCAAGAAGAGGCCCTGGGCCTGGTGGGTGCGCAGGCTCCTA 718

Qy      3975 C-----CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGG 4010
          |
Db     719  CTA CTGAGGAGCAGGAGGCTGCTGTCTCCTCCTCCTCTCCTCTGGTCCCTGGCACCTGG 778

Qy      4011 AGGAGGTGCCCAGTGTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCCT 4070
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Db	779	AGGAAGTGCCTGCTGCTGAGTCAGCAGGTCCTCCCCAGAGTCCTCAGGGAGCCTCTGCCT	838
Qy	4071	TTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCAGCAGCCGTG	4130
Db	839	TACCCACTACCATCAGCTTCACTTGTGAGGCAACCCAATGAGGGTTCAGCAGCCAAG	898
Qy	4131	AAGAGGAGGGGCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCGAGCAGTAATCACTA	4190
Db	899	AAGAGGAGGGGCCAAGCACCTCGCTGACGCAGAGTCCTTGTTCGAGAAGCACTCAGTA	958
Qy	4191	AGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCA	4250
Db	959	ACAAGGTGGATGAGTTGGCTCATTTTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCA	1018
Qy	4251	CAAAGGCAGAAATGCTGGAGAGTGTCAATCAAAAATTACAAGCACGTGTTTTCCTGAGATCT	4310
Db	1019	CAAAGGCAGAAATGCTGGAGAGAGTCAATCAAAAATTACAAGCGCTGCTTTCCTGTGATCT	1078
Qy	4311	TCGGCAAAGCCTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACC	4370
Db	1079	TCGGCAAAGCCTCCGAGTCCCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACC	1138
Qy	4371	CCACCGGCCACTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGG	4430
Db	1139	CCACCGGCCACTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGG	1198
Qy	4431	GTGATAATCAGATCATGCCAAGACAGGCTTCCTGATAATTGTCTGGTCATGATTGCAA	4490
Db	1199	GTAATAATCAGATCTTTCCCAAGACAGGCTTCCTGATAATCGTCTGGGCACAATTGCAA	1258
Qy	4491	TGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGT	4550
Db	1259	TGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGGGTGTGATGGGGGTGT	1318
Qy	4551	ATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGG	4610
Db	1319	ATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGG	1378
Qy	4611	TGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGT	4669
Db	1379	TGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGT	1438
Qy	4670	TCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGA	4729
Db	1439	TCCTGTGGGGTCCAAGGGCTCTGGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGA	1498
Qy	4730	TCAAGGTCAGTGCAAGAGTTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAG	4789
Db	1499	TCAGGGTCAATGCAAGAGTTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGTTAG	1558
Qy	4790	AGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGG---GGACT	4845
Db	1559	AGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGGCTGTGGGGAAGGGGCAGGGCT	1618
Qy	4846	GGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGG	4905
Db	1619	GGGCCAGTGCATCTAACA--GCCCTGTGCAGCAGCTTCCCTTGCCCTCGTGTGACATGAGG	1676
Qy	4906	CCCATTCCTTCACTC----TGAAGAGAGCGGTGAGTGTTCAGTAGTAGGTTTCTGTTCT	4961
Db	1677	CCCATTCCTTCACTCCTGTTTGAAGAAAAATAGTCAGTGTTCCTTAGTAGTGGGTTTCTATTTT	1730





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;      ADDRESSEE: Felfe & Lynch
;      STREET: 805 Third Avenue
;      CITY: New York City
;      STATE: New York
;      ZIP: 10022
;
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
;      COMPUTER: IBM
;      OPERATING SYSTEM: PC-DOS
;      SOFTWARE: Wordperfect
;
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/11/253,240
;      FILING DATE: 17-Oct-2005
;      CLASSIFICATION:
;
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US/09/579,543
;      FILING DATE: 26-May-2000
;      APPLICATION NUMBER: 09/583,850
;      FILING DATE:
;      APPLICATION NUMBER: PCT/US92/04354
;      FILING DATE: 22-MAY-1992
;      APPLICATION NUMBER: 07/807,043
;      FILING DATE: 12-DECEMBER-1991
;      APPLICATION NUMBER: 07/764,365
;      FILING DATE: 23-SEPTEMBER-1991
;      APPLICATION NUMBER: 07/728,838
;      FILING DATE: 9-JULY-1991
;      APPLICATION NUMBER: 07/705,702
;      FILING DATE: 23-MAY-1991
;
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Hanson, Norman D.
;      REGISTRATION NUMBER: 30,946
;      REFERENCE/DOCKET NUMBER: LUD 5353
;
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (212) 688-9200
;      TELEFAX: (212) 838-3884
;
;      INFORMATION FOR SEQ ID NO: 17:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 2305 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;      MOLECULE TYPE: genomic DNA
;      FEATURE:
;      NAME/KEY: MAGE-51 gene
;      SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-11-253-240-17

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Query Match          26.5%;  Score 1504.6;  DB 8;  Length 2305;
Best Local Similarity 83.7%;  Pred. No. 0;
Matches 1942;  Conservative 0;  Mismatches 304;  Indels 75;  Gaps 18;

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Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
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Db      1  GGATCCAGGCCCTGCCAGGAGAAAGGTGAGGGCCCTGTGTGAGCACAGAGGGGACCATTC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTACACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
         ||  ||  ||  |||  ||  |||||  |||||  |||||  |||||  |||  |
Db      61  ACCCCAAGAGGGTGGAGACCTCACAGATTCCAGCCTACCCTCCTGTTAGCACTGGGGGCC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 3435

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[illegible]

Db	1020	TCAAGGAGCCGGTCACAAAGGCAGAAATGCTGGAGAGCGTCATCAAAAATTACAAGCGCT	1079
Qy	4296	GTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACG	4355
Db	1080	GCTTTCTTGAGATCTTCGGCAAAGCCTCCGAGTCCTTGACGCTGGTCTTTGGCATTGACG	1139
Qy	4356	TGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCT	4415
Db	1140	TGAAGGAAGCGGACCCACAGCAACACCTACACCCTTGTCACCTGCCTGGGACTC--CT	1197
Qy	4416	ATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCC	4475
Db	1198	ATGATGGCCTGGTGGTT--TAATCAGATCATGCCCAAGACGGGCCTCTGATAATCGTCT	1255
Qy	4476	TGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGA	4535
Db	1256	TGGGCATGATTGCAATGGAGGGCAAATGCGTCCCTGAGGAGAAAATCTGGGAGGAGCTGG	1315
Qy	4536	GTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGC	4595
Db	1316	GTGTGATGAAGGTGTATGTTGGGAGGGAGCACAGTGTCTGTGGGGAGCCCAGGAAGCTGC	1375
Qy	4596	TCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGGCAGGTGCCCGACAGTGATCC	4655
Db	1376	TCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGCAGGTGCCCGACAGTGATCC	1435
Qy	4656	CGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGT	4715
Db	1436	CATATGCTATGAGTTACTGTGGGGTCCAAGGGCACTCGCTGC-----TTGAAAGT	1485
Qy	4716	CCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGA	4775
Db	1486	ACTGGAGCACGTGGTCAGGGTCAATGCAAGAGTTCCTCATTTCCATCCCTGCATGA	1545
Qy	4776	AGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGG	4835
Db	1546	AGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGCTGCAGCCAGGGCCACTGC	1605
Qy	4836	GAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCC-TCGT	4894
Db	1606	GAGGGGGGCTGGGCCAGTGCACCTTCCAGGGCTCCGTCCAGTAGTTTCCCCTGCTTAAT	1665
Qy	4895	GTGACATGAGGCCCATTCTTCACTC--TGAAGAGAGCGGTGAGTGTCTCAGTAGTAGGT	4952
Db	1666	GTGACATGAGGCCCATTCTTCTCTCTTTGAAGAGAGCAGTCAACATTCTTAGTAGTGGGT	1725
Qy	4953	TTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGAATTGTTCAAATG	5012
Db	1726	TTCTGTTCTATTGGATGACTTTGAGATTTGTCTTTGTTTCTTTTGAATTGTTCAAATG	1785
Qy	5013	TTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGTTTATGAATGACAGCAGTC	5072
Db	1786	-TTCTTTTAATGGGTGGTTGAATGAACCTCAGCATTCAAATTTATGAATGACAGTAGTC	1844
Qy	5073	ACAC--AGTTCGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGA	5130
Db	1845	ACACATAGTGCTGTTTATATAGTTTAGGAGTAAGAGTCTTGTTTTTATTTCAGATTGGGA	1904
Qy	5131	AATCCATTCTATTTTGTGAATTGGG--ATAATAACAGCAGTGGAATAAGTACTTA-GAAA	5187
Db	1905	AATCCATTCCATTTTGTGAATTGGGACATAGTTACAGCAGTGGAATAAGTATTCTTTAG	1964

Qy	5188	TGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCA	5247
Db	1965	AAATGTGAATGAGCAGTAAACTGATGAGA-----TAAAGAAATTAAGATATTTA	2016
Qy	5248	ATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAA--TTTTTAAAGATATATGCATACCTG	5305
Db	2017	ATTCTTGCCCTTATA-CTCAGTCTATTTCGGTAAAAATTTTTTTTTTAAAAATGTGCATACCTG	2075
Qy	5306	GATTTCCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAAGAATTCTTCCT	5365
Db	2076	GATTTCCCTTGGCTTCTTTGAGAATGTAAGACAAATTAATCTGAATAAATCATTCTCCCT	2135
Qy	5366	GTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAAGGCCCTGGGTT	5425
Db	2136	GTTCACTGGCTCATTTATTCTCTATGCACTGAGCATTTGCTCTGTGGAAGGCCCTGGGTT	2195
Qy	5426	AGTAGTGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAG	5485
Db	2196	AATAGTGAGATGCTAAGGTAAGCCAGACTCACCCCTACCCACAGGGTAGTAAAGTCTAG	2255
Qy	5486	GAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAA	5526
Db	2256	GAGCAGCAGTCATATAATTAAGGTGGAGAGATGCCCTCTAA	2296

US-11-253-240-16

; Sequence 16, Application US/11253240

; GENERAL INFORMATION:

APPLICANT: Gaugler, Batrice; Van den Eynde, BenoEt;  
van der Bruggen, Pierre; Boon-Falleur, Thierry

TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For

Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof

```
; NUMBER OF SEQUENCES: 30
```

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

; CITY: New York City

STATE: New York

; ZIP: 10022

; COMPUTER READABLE FORM:

```
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
```

```
;          COMPUTER:  IBM
```

```

;      OPERATING SYSTEM: PC-DOS

```

```
; SOFTWARE: Wordperfect
```

```

; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/11/253,240

; FILING DATE: 17-Oct-2005

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/579,543

FILING DATE: 26-May-2000

APPLICATION NUMBER: 09/583,850

; FILING DATE:

; APPLICATION NUMBER: PCT/US92/04354

; FILING DATE: 22-MAY-1992

APPLICATION NUMBER: 07/807,043

; FILING DATE: 12-DECEMBER-1991

```

;          FILING DATE: 23-SEPTEMBER-1991
;          APPLICATION NUMBER: 07/728,838
;          FILING DATE: 9-JULY-1991
;          APPLICATION NUMBER: 07/705,702
;          FILING DATE: 23-MAY-1991
;
;  ATTORNEY/AGENT INFORMATION:
;          NAME: Hanson, Norman D.
;          REGISTRATION NUMBER: 30,946
;          REFERENCE/DOCKET NUMBER: LUD 5353
;
;  TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (212) 688-9200
;          TELEFAX: (212) 838-3884
;
;  INFORMATION FOR SEQ ID NO: 16:
;          SEQUENCE CHARACTERISTICS:
;              LENGTH: 2226 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;          MOLECULE TYPE: genomic DNA
;          FEATURE:
;              NAME/KEY:     MAGE-5 gene
;          SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-11-253-240-16

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Query Match          24.9%;  Score 1410.8;  DB 8;  Length 2226;
Best Local Similarity 81.4%;  Pred. No. 0;
Matches 1874;  Conservative 0;  Mismatches 312;  Indels 116;  Gaps 16;

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Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
          ||||| ||||| ||| | ||||| ||||| ||||| ||| |
Db      1 GGATCCAGGCCCTGCCAGGAGAAAGGTGAGGGCCCTGTGTGAGCACAGAGGGGACCATTC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTGGTAGCACTGAGAAGC 3375
          || || || ||| ||| || ||||| ||||| ||||| ||||| ||| |
Db      61 ACCCCAAGAGGGTGGAGACCTCACAGATTCCAGCCTACCCTCCTGTTAGCACTGGGGGCC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 3435
          ||||| ||||| ||||| ||||| || || ||||| ||||| |||||
Db      121 TGAGGCTGTGCTTGCACTCTGCACCCTGAGGGCCCATGCATTCTCTTCAGGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          |||| ||| || ||||| ||||| || || ||||| ||||| |||||
Db      181 GGAAACAGACACTGAGGCCCTTGGTCTGAGGCCGTGCCCTCAGGTCACAGAGCAGAGGAGA 240

Qy      3496 CACAG----GGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCT 3551
          ||| ||||| ||||| ||||| ||||| ||||| || |||||
Db      241 TGCAGACGTCTAGTGCCAGCAGTGAACGTTTGCTTGAATGCACACTAATGGCCCCCATC 300

Qy      3552 GCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCA-CCTCCCTACTGTAGTCTCTGT 3610
          ||| ||| ||| || ||||| || ||||| ||||| ||||| |||||
Db      301 GCCCCAGAACATATGGGACTCCAGAGCACCTGGCCTCACCTCTCTACTGTAGTCTCTGC 360

Qy      3611 AGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTT 3670
          ||||| ||||| || || || || ||||| ||||| |||||
Db      361 AGAATCAGCCTCTGCTTGCTTGTTGCTACCCTGAGGTGCCCTCTCACTTTTTCCTTCAGGTT 420

Qy      3671 TTCAGGGGACAGGCCAACCCAGAGGAC-----AGGATTCCCTGGAGGCCACA 3717
          ||||| ||||| ||| || || ||||| ||||| ||||| ||
Db      421 CTCAGGGGACAGGCTGACCAGGATCACCAGGAAGCTCCAGAGGATCCCCAGGAGGCCCTA 480

Qy      3718 GAGGAGCACC-AAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGT 3776

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Db	481	GAGGAGCACCAAAGGAGAAGATCTGTAAGTAAGCCTTTGTTAGAGCCTCCAAGGTTTCAGT	540
Qy	3777	TCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCC	3836
Db	541	TTTTAGCTGAGGCTTCTCACATGCTCCCTCTCTCTCCAGGCCAGTGGGTCTCCATTGCCC	600
Qy	3837	AGCTCCTGCCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGA	3896
Db	601	AGCTCCTGCCCCACACTCCTGCCTGTTGCGGTGACCAGAGTCGTCATGTCTCTTGAGCAGA	660
Qy	3897	GGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG	3956
Db	661	AGAGTCAGCACTGCAAGCCTGAGGAA-----	686
Qy	3957	TGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGG	4016
Db	687	-----CTCCTCTGGTCCCAGGCACCTGGGGGAGG	716
Qy	4017	TGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCA	4076
Db	717	TGCCTGCTGCTGGGTCAACAGGTCTCTCAAGAGTCCTCAGGGAGCCTCCGCCATCCCCA	776
Qy	4077	CTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGG	4136
Db	777	CTGCCATCGATTTCACCTCTATGGAGGCAATCCATTAAGGGCTCCAGCAACCAAGAAGAGG	836
Qy	4137	AGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGG	4196
Db	837	AGGGGCCAAGCACCTCCCCTGACCCAGAGTCTGTGTTCCGAGCAGCACTCAGTAAGAAGG	896
Qy	4197	TGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGG	4256
Db	897	TGGCTGACTTGATTTCATTTCTGCTCCTCAAGTATTAAGTCAAGGAGCTGGTCACAAAGG	956
Qy	4257	CAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCA	4316
Db	957	CAGAAATGCTGGAGAGCGTCATCAAAAATTACAAGCGCTGCTTTCTTGAGATCTTCGGCA	1016
Qy	4317	AAGCCTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCG	4376
Db	1017	AAGCCTCCGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCGGACCCACCA	1076
Qy	4377	GCCACTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTG---	4433
Db	1077	GCAACACCTACACCTTGTCACCTGCCTGGG--ACTCCTATGATGGCTGCTGGTTGATA	1134
Qy	4434	ATAATCAGATCATGCCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGG	4493
Db	1135	ATAATCAGATCATGCCCCAAGACGGGCCTCCTGATAATCGTCTTGGGCATGATTGCAATGG	1194
Qy	4494	AGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATG	4553
Db	1195	AGGGCAAATGCGTCCCTGAGGAGAAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGTATG	1254
Qy	4554	ATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGC	4613
Db	1255	TTGGGAGGGAGCACAGTGTCTGTGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGC	1314
Qy	4614	AGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCC	4672

Db	1315	AGGAAAAC TACCTGGAGTACCGGCAGGTGCCCAGCAGTGATCCCATATGCTATGAGTTAC	1374
Qy	4673	TGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCA	4732
Db	1375	TGTGGGGTCCAAGGGCACTCGCTG-----CTTGAAAGTACTGGAGCACGTGGTCA	1424
Qy	4733	AGGTCAGTGCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGG	4792
Db	1425	GGGTCAATGCAAGAGTTCTCATTTCTACCCATCCCTGCGTGAAGCAGCTTTGAGAGAGG	1484
Qy	4793	AGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAG	4851
Db	1485	AGGAAGAGGGAGTCTGAGCATGAGCTGCAGCCAGGGCCACTGCGAGGGGGGCTGGGCCAG	1544
Qy	4853	TGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCC-TCGTGTGACATGAGGCCCAT	4911
Db	1545	TGCACCTTCCAGGGCTCCGTCCAGTAGTTTCCCCTGCCTTAATGTGACATGAGGCCCAT	1604
Qy	4912	CTTCACTC--TGAAGAGAGCGGTCAAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTG	4969
Db	1605	CTTCTCTCTTTGAAGAGAGCAGTCAACATTCCTTAGTAGTGGGTTTCTGTTCTATTGGATG	1664
Qy	4970	ACTTGGAGATTTATCTTTGTTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTAAGGGATG	5029
Db	1665	ACTTTGAGATTTGTCTTTGTTTCCTTTTGGAAATTGTTCAAATGTTTC-TTTAATGGGTG	1723
Qy	5030	GTTGAATGAAC TTCAGCATCCAAGTTTATGAATGACAGCAGTCACAC--AGTCTGTGTA	5087
Db	1724	GTTGAATGAAC TTCAGCATTCAAATTTATGAATGACAGTAGTCACACATAGTGCTGTTTA	1783
Qy	5088	TATAGTTTAAGGGTAAGAGTCTTGTTTATTTCAGATTGGGAAATCCATTCTATTTTGT	5147
Db	1784	TATAGTTTAGGAGTAAGAGTCTTGTTTTTATTTCAGATTGGGAAATCCATTCCATTTTGT	1843
Qy	5148	GAATTGGG--ATAATAACAGCAGTGGAAATAAGTACTTA-GAAATGTGAAAAATGAGCAGT	5204
Db	1844	GAATTGGGACATAGTTACAGCAGTGGAAATAAGTATTCATTTAGAAATGTGAATGAGCAGT	1903
Qy	5205	AAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCT	5264
Db	1904	AAAAC TGATGACA-----TAAAGAAAT TAAAAGATATTTAATTCTTGCTTATACTCA	1955
Qy	5265	CAGTCTATTCTGTAAAATTTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTG	5324
Db	1956	GTCTATTTCGGTAAAATTTTTTTTTTAAAAAATGTGCATACCTGGATTTCCTTGGCTTCTTTG	2015
Qy	5325	AGAATGTAAGAGAAATTAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTT	5384
Db	2016	AGAATGTAAGACAAATTAATCTGAATAAATCATTCTCCCTGTTCACTGGCTCATTAT	2075
Qy	5385	CTCCATGCACTGAGCATCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGG	5444
Db	2076	CTCTATGCACTGAGCATTGCTCTGTGGAAGGCCCTGGGTTAATAGTGAGATGCTAAGG	2135
Qy	5445	TAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATC	5504
Db	2136	TAAGCCAGACTCACCCCTACCCACAGGGTAGTAAAGTCTAGGAGCAGCAGTCATATAATT	2195
Qy	5505	GAGGTGGCAAGATGTCTCTTAA	5526
Db	2196	AAGGTGGAGAGATGCCCTCTAA	2217

RESULT 12  
 US-11-266-748A-87851  
 ; Sequence 87851, Application US/11266748A  
 ; Publication No. US20060134663A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harkin, Paul  
 ; APPLICANT: Johnston, Patrick  
 ; APPLICANT: Mulligan, Karl  
 ; TITLE OF INVENTION: Transcriptome Microarray Technology and  
 ; TITLE OF INVENTION: Methods of Using the Same  
 ; FILE REFERENCE: 55815-0102 (319189)  
 ; CURRENT APPLICATION NUMBER: US/11/266,748A  
 ; CURRENT FILING DATE: 2005-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105479.2  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105482.6  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105483.4  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105507.0  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105485.9  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105484.2  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: US 60/662,276  
 ; PRIOR FILING DATE: 2005-03-14  
 ; PRIOR APPLICATION NUMBER: US 60/700,293  
 ; PRIOR FILING DATE: 2005-07-18  
 ; NUMBER OF SEQ ID NOS: 483996  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 87851  
 ; LENGTH: 1577  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 US-11-266-748A-87851

Query Match 20.9%; Score 1188.2; DB 8; Length 1577;  
 Best Local Similarity 89.4%; Pred. No. 4.1e-299;  
 Matches 1390; Conservative 0; Mismatches 133; Indels 32; Gaps 9;

Qy	3816	GCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAG	3875
Db	40	GCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGTTGCCCTGACGAGAG	99
Qy	3876	TCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCC	3935
Db	100	TCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCC	159
Qy	3936	AACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCTCCTCTGG	3995
Db	160	AACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCGCCTCCTCCTCTCCTCTGG	219
Qy	3996	TCCTGGGCACCTGGAGGAGGTGCCCAGTCTGGGTCAACAGATCCTCCCCAGAGTCCTC	4055
Db	220	TCCTGGGCACCTGGAGGAGGTGCCCAGTCTGGGTCAACAGATCCTCCCCAGAGTCCTC	279
Qy	4056	AGGGAGCCTCCGCCTTTCCTCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGG	4115



Db	280	AGGGAGCCTCCGCTTTCCCACTACCATCAACTTCACTCAACAGAGGCAACCCAGTGAGG	339
Qy	4116	GTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTC	4175
Db	340	GTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTC	399
Qy	4176	GAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTTCTGCTCCTCAAATATCGAG	4235
Db	400	GAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTTCTGCTCCTCAAATATCGAG	459
Qy	4236	CCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACT	4295
Db	460	CCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACT	519
Qy	4296	GTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACG	4355
Db	520	GTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACG	579
Qy	4356	TGAAGGAAGCAGACCCACCGGCCACTCCTATGTCTTGTACCTGCCTAGGTCTCTCCT	4415
Db	580	TGAAGGAAGCAGACCCACCGGCCACTCCTATGTCTTGTACCTGCCTAGGTCTCTCCT	639
Qy	4416	ATGATGGCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCTTGATAATTGTCC	4475
Db	640	ATGATGGCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCTTGATAATTGTCC	699
Qy	4476	TGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGA	4535
Db	700	TGGTCATGATCGCAATAGAGGGCGGCTGTGCCCTGAGGAGGAAATCTGGGAGGAGCTGA	759
Qy	4536	GTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGC	4595
Db	760	GTATGTTGGAGGTGTATGAGGGGAAGGAGGACAGTGTCTTCGCACATCCCAGGAAGCTGC	819
Qy	4596	TCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATC	4654
Db	820	TCATGCAAGATCTGGTGCAGGAAAAC TACCTGGAGTACCGGCAGGTGCCGGGCAGTGATC	879
Qy	4655	CCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAG	4714
Db	880	CTGCATGCTACGAGTTCTGTGGGGTCCAAGGGCCCTCATTGAAACCAGCTATGTGAAAG	939
Qy	4715	TCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTG	4774
Db	940	TCCTGCACCATACTAAAGATCGGTGAAGAACCTCACATTTCTACCCACCCCTGCATG	999
Qy	4775	AAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTG	4834
Db	1000	AACGGGCTTTGAGAGAGGGAGAAGAGTGAGTCTCAGCACAAAGTTGCAGCCAAGGCCAGTG	1059
Qy	4835	GGAGGGGGACTGGGCCAGTGCACCTCCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGT	4894
Db	1060	GGAGGGGGACTGGGCCAGTGCACCTCCAGGGACCCATCCAGCAACTTCCACTGCCTCGA	1119
Qy	4895	GTGACATGAGGCCCATTCCT--CACTCTGAAGAGAGCGGTGAGTGTTCTCAGTAGTAGGT	4952
Db	1120	GTGACATGAGGCCCATTCCTGCCTCTTTGAAGAGAGCAGTCAGCATTCCTTAGCAGTGAGT	1179
Qy	4953	TTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGAAATTGTTCAAATG	5012
Db	1180	TTCTGTTCTGTTGGATGACTTTGAGATTTATCTTTGTTTCTGTTGGAATTGTTCAAATG	1239

```

Qy      5013 TTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGTTTATGAATGACAGCAGTC 5072
        ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1240 TTCC-TTTTAACAAATGGTTGGATGAAC TTCAGCATCCAAGTTTATGAATGACAGTAGTC 1298

Qy      5073 ACAC--AGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGA 5130
        ||||  |||  ||||  |||||  |||||  |||||  |||  |||||  |||||  |||||
Db      1299 ACACATAGTGCTGTTTATATAGTTTAGGGGTAAGAGTCCTGTTTTTTATTTCAGATTGGGA 1358

Qy      5131 AATCCATTCTATTTTGTGAATTG--GGATAATAACAGCAGTGGAATAAGTACTTAGAAAT 5188
        |||||  |||||  |||||  ||||  |||||  |||||  |||||  |||||  ||||  ||
Db      1359 AATCCATTCCATTTTGTGAGTTGTCACATAATAACAGCAGTGGAATATGTATTGCGCTAT 1418

Qy      5189 GT----GAAAAATGAGCAGTAAAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAG 5244
        |  |  |  |||  |||||  |||||  ||||  |  ||  ||||  |  ||  |||||
Db      1419 ATTGTGAACGAATTAGCAGTAAAAATACATGATACAAGGAAC-----TCAAAAGATAG 1470

Qy      5245 TCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTTAAAGATATATGCATACCT 5304
        |  |||||  |||||  |||||  |||||  |||||  |||||  |||||  ||||  |||
Db      1471 TTAATTCTTGCCTTATACCTCAGTCTATTATGTAAAA--TTAAAAATATGTGTA----- 1522

Qy      5305 GGATTTCTTGGCTTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAAGAATT 5359
        |  ||  |||||  |||||  |||||  |||||  |||||  |||||  ||  ||||
Db      1523 ----TGTTTTTGCTTCTTTGAGAATGCAAAAGAAATTAATCTAGGTAGGTAATT 1573

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# RESULT 13

```

US-11-266-748A-112460
; Sequence 112460, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 112460
; LENGTH: 1577
; TYPE: DNA
; ORGANISM: Homo Sapiens

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—

Matches 1390; Conservative 0; Mismatches 133; Indels 32; Gaps 9;

Db 820 TCATGCAAGATCTGGTGCAGGAAAACCTACCTGGAGTACCGGCAGGTGCCGGGCAGTGATC 879

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Qy      4655 CCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAG 4714
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      880 CTGCATGCTACGAGTTCCTGTGGGGTCCAAGGGCCCTCATTGAAACCAGCTATGTGAAAG 939

Qy      4715 TCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTG 4774
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      940 TCCTGCACCATACTAAAGATCGGTGAAGAACCTCACATTTCTTACCCACCCCTGCATG 999

Qy      4775 AAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTG 4834
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1000 AACGGGCTTTGAGAGAGGGAGAAGAGTGAGTCTCAGCACAAGTTGCAGCCAAGGCCAGTG 1059

Qy      4835 GGAGGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCTCCAGCAGCTTCCCTGCCTCGT 4894
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1060 GGAGGGGGGACTGGGCCAGTGCACCTTCCAGGGACCCATCCAGCAACTTCCACTGCCTCGA 1119

Qy      4895 GTGACATGAGGCCCATTCCTT--CACTCTGAAGAGAGCGGTCAAGTGTCTCAGTAGTAGGT 4952
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1120 GTGACATGAGGCCCATTCCTGCCTCTTTGAAGAGAGCAGTCAGCATTCTTAGCAGTGAGT 1179

Qy      4953 TTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGAAATTGTTCAAATG 5012
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1180 TTCTGTTCTGTTGGATGACTTTGAGATTTATCTTTGTTTCTGTTGGAATTGTTCAAATG 1239

Qy      5013 TTTTTTTTTTAAGGGATGGTTGAATGAACCTTCAGCATCCAAGTTTATGAATGACAGCAGTC 5072
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1240 TTCC-TTTTAACAAATGGTTGGATGAACCTTCAGCATCCAAGTTTATGAATGACAGTAGTC 1298

Qy      5073 ACAC--AGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTCAGATTGGGA 5130
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1299 ACACATAGTGCTGTTTATATAGTTTAGGGTAAGAGTCCTGTTTTTATTCAGATTGGGA 1358

Qy      5131 AATCCATTCTATTTTGTGAATTG--GGATAATAACAGCAGTGGAATAAGTACTTAGAAAT 5188
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1359 AATCCATTCCATTTTGTGAGTTGTCACATAATAACAGCAGTGGAATATGTATTTGCCTAT 1418

Qy      5189 GT----GAAAAATGAGCAGTAAAATAGATGAGATAAAGAAC TAAAGAAATTAAGAGATAG 5244
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1419 ATTGTGAACGAATTAGCAGTAAAATACATGATACAAGGAAC-----TCAAAAGATAG 1470

Qy      5245 TCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATATGCATACCT 5304
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1471 TTAATTCTTGCCTTATACCTCAGTCTATTATGTAAAA---TTAAAAATATGTGTA----- 1522

Qy      5305 GGATTTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAGAATT 5359
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1523 ----TGTTTTTGCTTCTTTGAGAATGCAAAAGAAATTAAATCTAGGTAGGTAATT 1573

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RESULT 14

US-11-266-748A-140662/c

; Sequence 140662, Application US/11266748A

; Publication No. US20060134663A1

; GENERAL INFORMATION:

; APPLICANT: Harkin, Paul

; APPLICANT: Johnston, Patrick

; APPLICANT: Mulligan, Karl

; TITLE OF INVENTION: Transcriptome Microarray Technology and

; TITLE OF INVENTION: Methods of Using the Same

; FILE REFERENCE: 55815-0102 (319189)

```

; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 140662
; LENGTH: 1577
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-140662

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Query Match          20.9%; Score 1188.2; DB 8; Length 1577;
Best Local Similarity 89.4%; Pred. No. 4.1e-299;
Matches 1390; Conservative 0; Mismatches 133; Indels 32; Gaps 9;

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Qy      3816 GCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAG 3875
          |||
Db      1538 GCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGTTGCCCTGACGAGAG 1479

Qy      3876 TCATCATGTCTCTTGAGCAGAGGAGTCTGCAAGCCTGAGGAAGCCCTTGAGGCCC 3935
          |||
Db      1478 TCATCATGTCTCTTGAGCAGAGGAGTCTGCAAGCCTGAGGAAGCCCTTGAGGCCC 1419

Qy      3936 AACAAAGAGGCCCTGGGCCTGGTGTGTGTGTCAGGCTGCCACCTCCTCCTCTCCTCTGG 3995
          |||
Db      1418 AACAAAGAGGCCCTGGGCCTGGTGTGTGTGTCAGGCTGCCGCCTCCTCCTCTCCTCTGG 1359

Qy      3996 TCCTGGGCACCTGGAGGAGGTGCCCCTGCTGGGTCAACAGATCCTCCCCAGAGTCCTC 4055
          |||
Db      1358 TCCTGGGCACCTGGAGGAGGTGCCCCTGCTGGGTCAACAGATCCTCCCCAGAGTCCTC 1299

Qy      4056 AGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGG 4115
          |||
Db      1298 AGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCAACAGAGGCAACCCAGTGAGG 1239

Qy      4116 GTTCCAGCAGCCGTGAAGAGGAGGGGCAAGCACCTCTGTATCCTGGAGTCCTTGTTCC 4175
          |||
Db      1238 GTTCCAGCAGCCGTGAAGAGGAGGGGCAAGCACCTCTGTATCCTGGAGTCCTTGTTCC 1179

Qy      4176 GAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAG 4235
          |||
Db      1178 GAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAG 1119

Qy      4236 CCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACT 4295
          |||
Db      1118 CCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACT 1059

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Qy	4296	GTTTTTCCTGAGATCTTTCGGCAAAGCCTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACG	4355
Db	1058		
Qy	4356	TGAAGGAAGCAGACCCCCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCT	4415
Db	998		
Qy	4416	ATGATGGCCTGCTGGGTGATAATCAGATCATGCCAAGACAGGCTTCTTGATAATTGTCC	4475
Db	938		
Qy	4476	TGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGA	4535
Db	878		
Qy	4536	GTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGC	4595
Db	818		
Qy	4596	TCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATC	4654
Db	758		
Qy	4655	CCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAG	4714
Db	698		
Qy	4715	TCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTG	4774
Db	638		
Qy	4775	AAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTG	4834
Db	578		
Qy	4835	GGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCCCTCGT	4894
Db	518		
Qy	4895	GTGACATGAGGCCCCATTCTT--CACTCTGAAGAGAGCGGTGAGTGTCTCAGTAGTAGGT	4952
Db	458		
Qy	4953	TTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCTTTTGGAAATTGTTCAAATG	5012
Db	398		
Qy	5013	TTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGTTTATGAATGACAGCAGTC	5072
Db	338		
Qy	5073	ACAC--AGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGA	5130
Db	279		
Qy	5131	AATCCATTCTATTTTGTGAATTG--GGATAATAACAGCAGTGGAATAAGTACTTAGAAAT	5188
Db	219		

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Qy      5189 GT----GAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAG 5244
          |      |   ||| ||||| ||||| ||||| | || |||||
Db      159 ATTGTGAACGAATTAGCAGTAAAATACATGATACAAGGAAC-----TCAAAAGATAG 108

Qy      5245 TCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTTAAAGATATATGCATACCT 5304
          | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      107 TTAATTCTTGCCTTATACCTCAGTCTATTATGTAAAA--TTAAAAATATGTGTA----- 56

Qy      5305 GGATTTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAAGAATT 5359
          |   || ||||| ||||| || ||||| ||||| |||||
Db      55 ----TGTTTTTGCTTCTTTGAGAATGCAAAAGAAATTAATCTAGGTAGGTAATT 5

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RESULT 15

US-11-253-240-11

; Sequence 11, Application US/11253240

; Publication No. US20060127356A1

; GENERAL INFORMATION:

; APPLICANT: Gaugler, Batrice; Van den Eynde, BenoEt;  
 ; van der Bruggen, Pierre; Boon-Falleur, Thierry  
 ; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For  
 ; Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch  
 ; STREET: 805 Third Avenue  
 ; CITY: New York City  
 ; STATE: New York  
 ; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
 ; COMPUTER: IBM  
 ; OPERATING SYSTEM: PC-DOS  
 ; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/11/253,240  
 ; FILING DATE: 17-Oct-2005  
 ; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/579,543  
 ; FILING DATE: 26-May-2000  
 ; APPLICATION NUMBER: 09/583,850  
 ; FILING DATE:  
 ; APPLICATION NUMBER: PCT/US92/04354  
 ; FILING DATE: 22-MAY-1992  
 ; APPLICATION NUMBER: 07/807,043  
 ; FILING DATE: 12-DECEMBER-1991  
 ; APPLICATION NUMBER: 07/764,365  
 ; FILING DATE: 23-SEPTEMBER-1991  
 ; APPLICATION NUMBER: 07/728,838  
 ; FILING DATE: 9-JULY-1991  
 ; APPLICATION NUMBER: 07/705,702  
 ; FILING DATE: 23-MAY-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, Norman D.  
 ; REGISTRATION NUMBER: 30,946  
 ; REFERENCE/DOCKET NUMBER: LUD 5353

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200  
 ; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 11:

```

; SEQUENCE CHARACTERISTICS:
;     LENGTH: 1640 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
;     NAME/KEY: cDNA MAGE-3
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-11-253-240-11

```

Query Match 17.4%; Score 988.8; DB 8; Length 1640;  
 Best Local Similarity 81.5%; Pred. No. 4.4e-247;  
 Matches 1253; Conservative 0; Mismatches 252; Indels 33; Gaps 8;

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Qy      3816 GCCTGTGGGTCTTCATTGCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAG 3875
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      107 GCCAGTGGGTCTCCATTGCCAGCTCCTGCCCACACTCCCGCCTGTTGCCCTGACCAGAG 166

Qy      3876 TCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCC 3935
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      167 TCATCATGCCTCTTGAGCAGAGGAGTCAGCACTGCAAGCCTGAAGAAGGCCCTTGAGGCCC 226

Qy      3936 AACAAAGAGGCCCTGGGCCTGGTGTGTGTGCAAGGCT-----GCCA 3974
        | ||||| ||||| ||| ||||| ||
Db      227 GAGGAGAGGCCCTGGGCCTGGTGGGTGCGCAGGCTCCTGCTACTGAGGAGCAGGAGGCTG 286

Qy      3975 CCTCCTCCTCCTCTCCTCTGGTCCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAA 4034
        ||||| ||| ||| ||| | ||||| ||||| ||||| ||| | |||
Db      287 CCTCCTCCTCTCTACTCTAGTTGAAGTCACCCTGGGGGAGGTGCCTGCTGCCGAGTCAC 346

Qy      4035 CAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTC 4094
        ||||| ||||| ||||| ||||| ||| ||||| ||||| ||| | |||
Db      347 CAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCAGCCTCCCCACTACCATGAACCTACCCCTC 406

Qy      4095 GACAGAGGCAACCCAGTGAGGGTTCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTT 4154
        ||| ||| || ||||| ||||| || ||||| ||||| |||||
Db      407 TCTGGAGCCAATCCTATGAGGACTCCAGCAACCAAGAAGAGGAGGGGCCAAGCACCTTCC 466

Qy      4155 GTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTT 4214
        | ||||| ||||| ||||| ||| || ||||| || ||||| ||
Db      467 CTGACCTGGAGTCCGAGTTCCAAGCAGCACTCAGTAGGAAGGTGGCCGAGTTGGTTTCATT 526

Qy      4215 TTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTG 4274
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      527 TTCTGCTCCTCAAGTATCGAGCCAGGGAGCCGGTCACAAAGGCAGAAATGCTGGGGAGTG 586

Qy      4275 TCATCAAAAATTACAAGCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGC 4334
        || || ||||| || | ||||| ||||| ||||| || |||||
Db      587 TCGTCGGAATTGGCAGTATTTCTTTCTGTGATCTTCAGCAAAGCTTCAGTTCCTTGC 646

Qy      4335 AGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCTCTTG 4394
        ||||| ||||| || ||| ||||| ||||| ||||| || |||||
Db      647 AGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACTTGATACATCTTTG 706

Qy      4395 TCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGA 4454
        ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db      707 CCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAAGG 766

Qy      4455 CAGGCTTCCTGATAATGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGG 4514
        ||||| ||||| ||||| ||| || ||||| ||||| || |||||

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Db	767	CAGGCCTCCTGATAATCGTCTCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTTGAGG	826
Qy	4515	AGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCT	4574
Db	827	AGAAAATCTGGGAGGAGCTGAGTGTGTTAGAGGTGTTTGAGGGGAGGGAAGACAGTATGT	886
Qy	4575	ATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-C	4633
Db	887	TGGGGGATCCCAAGAAGCTGCTCACCCAACATTTCTGTGCAGGAAAACACCTGGAGTACC	946
Qy	4634	GGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCG	4693
Db	947	GGCAGGTCCCCGGCAGTGATCCTGCATGTTATGAATTCCTGTGGGGTCCAAGGGCCCTCG	1006
Qy	4694	CTGAAACCAGCTATGTGAAAGTCCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCT	4753
Db	1007	TTGAAACCAGCTATGTGAAAGTCCCTGCACCATATGGTAAAGATCAGTGGAGGACCTCACA	1066
Qy	4754	TTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCAT	4813
Db	1067	TTTCCTACCCACCCCTGCATGAGTGGGTTTGTGAGAGAGGGGAAGAGTGAGTCTGAGCAC	1126
Qy	4814	GAGTTGCAGCCAAGGCCAGTGAGGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTC	4873
Db	1127	GAGTTGCAGCCAGGGCCAGTGAGGGGGGTCTGGGCCAGTGCACCTTCCGGGGCCGCATC	1186
Qy	4874	CAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTC--TGAAGAGAGCGG	4931
Db	1187	CCTTAGTTTCCACTGCCTCCTGTGACGTGAGGCCCATTCCTTCACTCTTTGAAGCGAGCAG	1246
Qy	4932	TCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTC	4991
Db	1247	TCAGCATCTTAGTAGTGGGTTTCTGTTCTGTTGGATGACTTTGAGATTATCTTTGTTT	1306
Qy	4992	TCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCA	5051
Db	1307	CCTGTTGGAGTTGTTCAAATG-TTCCTTTTAACGGATGGTTGAATGAGCGTCAGCATCCA	1365
Qy	5052	AGTTTATGAATGACAGCAGTCACAC--AGTTCTGTGTATATAGTTTAAGGGTAAGAGTCT	5109
Db	1366	GGTTTATGAATGACAGTAGTCACACATAGTGCTGTTTATATAGTTTAGGAGTAAGAGTCT	1425
Qy	5110	TGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGG--ATAATAACAGCA	5167
Db	1426	TGTTTTTTACTCAAATTGGGAAATCCATTCCATTTTGTGAATTGTGACATAATAATAGCA	1485
Qy	5168	GTGGAATAAGTACTT-AGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACT	5226
Db	1486	GTGGTAAAAGTATTTGCTTAAAATGTGAGCGAATTAGCAATAACATACATGAGATAACT	1545
Qy	5227	AAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAATTTTT	5286
Db	1546	CAAGAAATCAAAGATAGTTGATTCTTGCCCTGTACCTCAATCTATTCTGTAAAA--TT	1602
Qy	5287	AAAGATATATGCATACCTGGATTTCCTTGCCCTTCTTTG	5324
Db	1603	AAACAAATATGCAAACCAGGATTTCTTGACTTCTTTG	1640

